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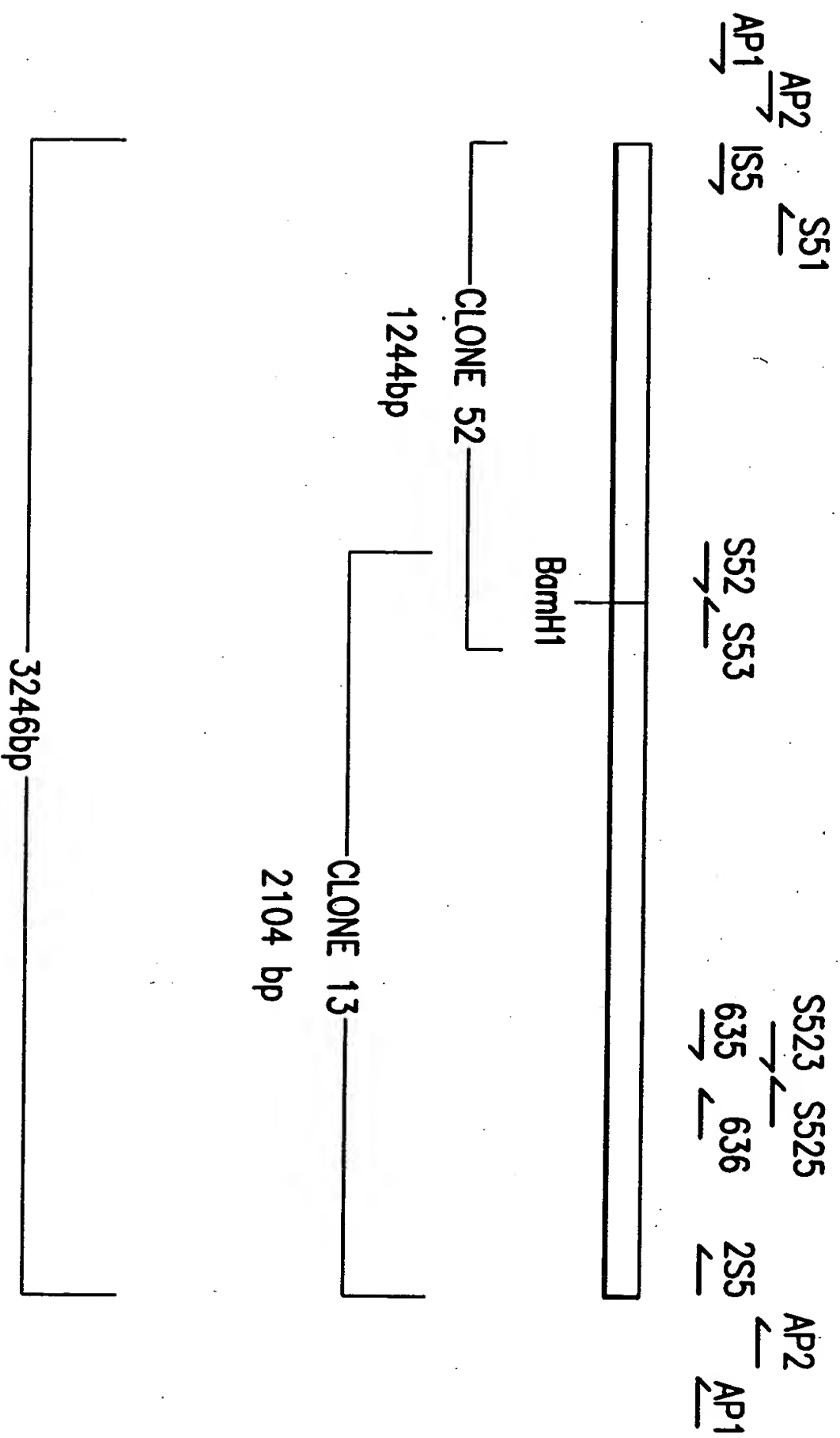
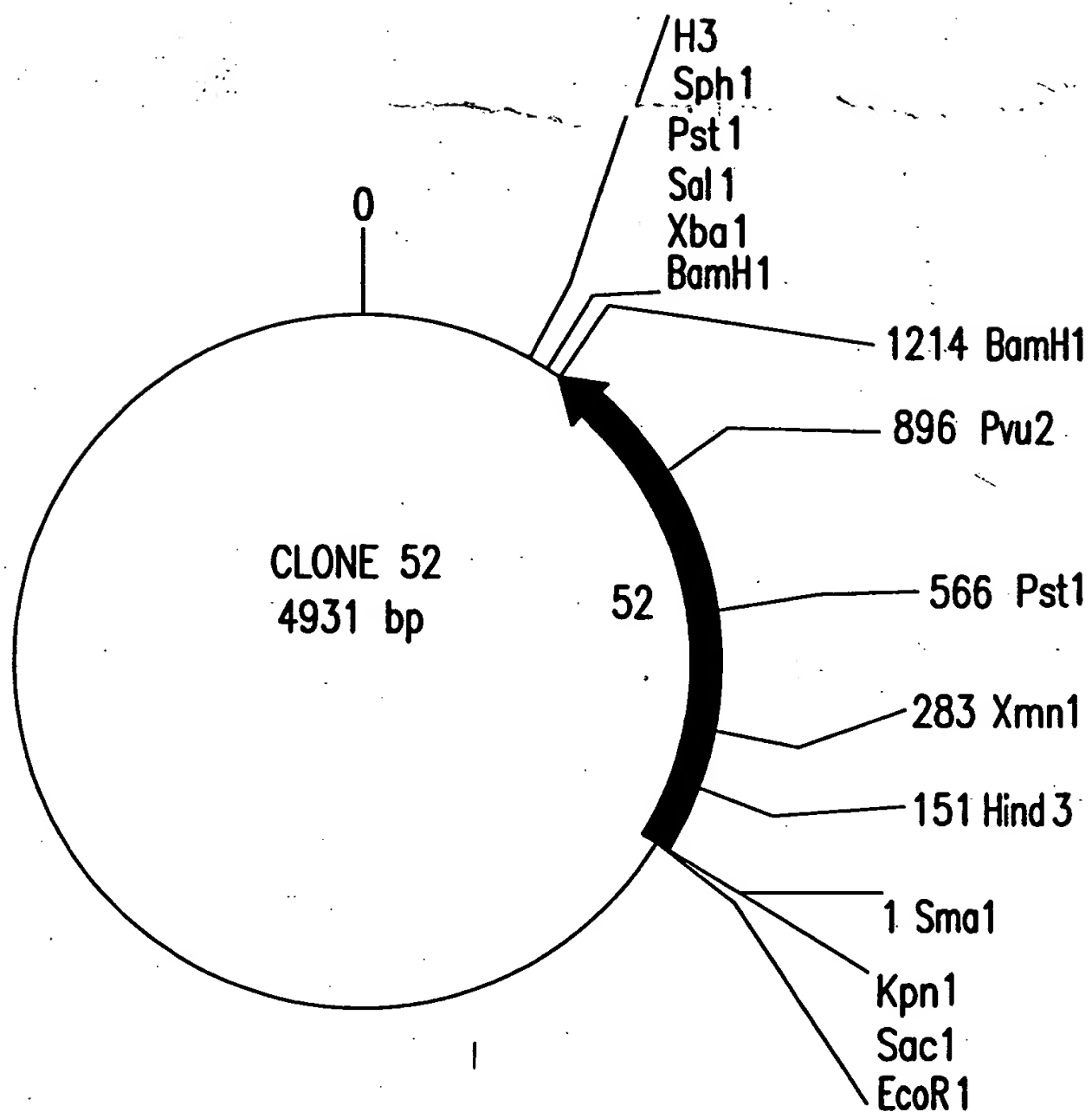
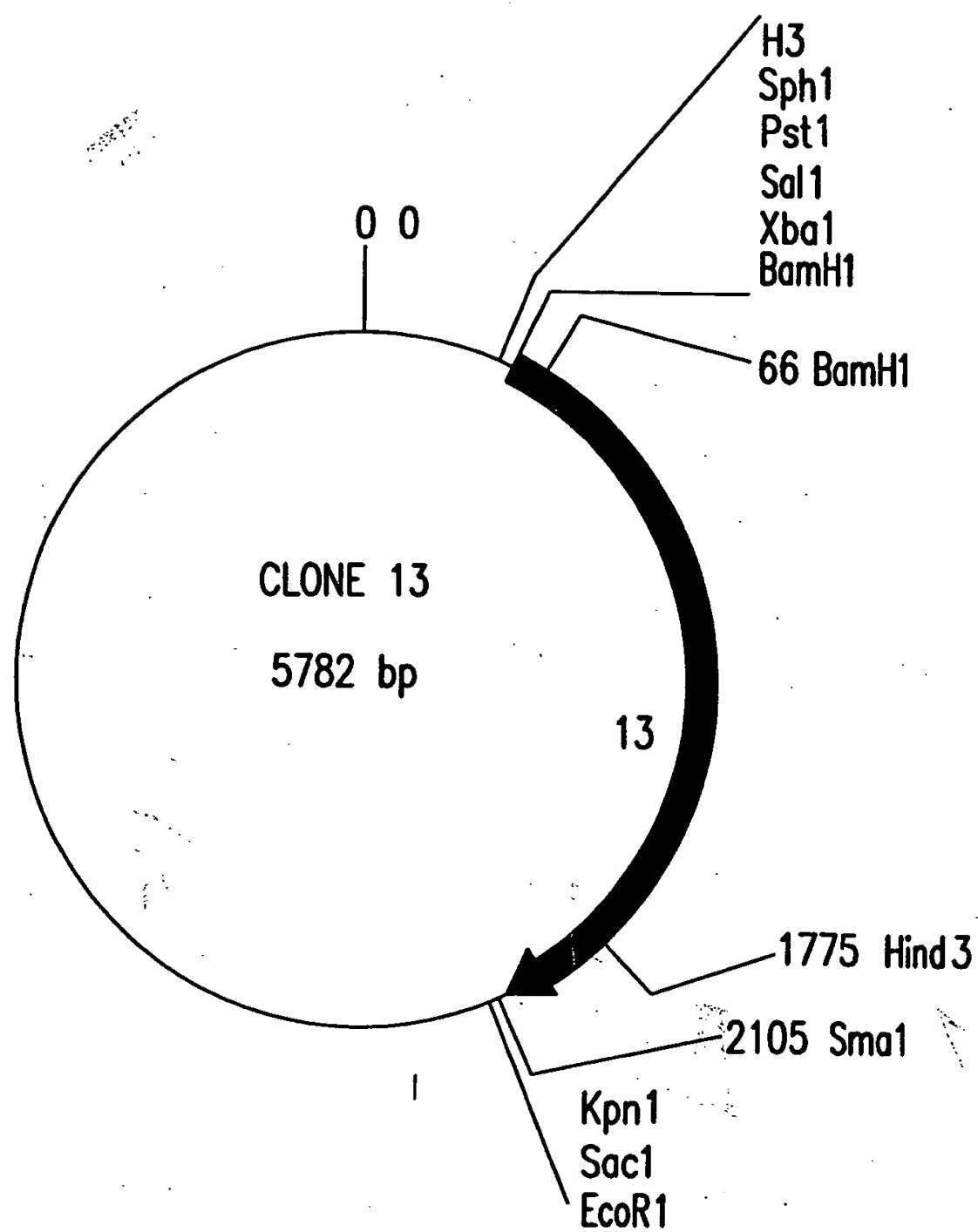


FIG. 1



COMMENTS/REFERENCES: 52=3' SIDE OF S5 (AtMSH3) 1244bp IN pUC18/Sma1

FIG.2



COMMENTS/REFERENCES: 13=3' SIDE OF S5 (AtMSH3) 2104bp IN pUC18/Sma1

FIG.3

1	cCTAAGAAAGCGCGGAAATTGGCAACCCAAGTTCGCCATAGCCACGACCAGACCTTCCAATTCTCTTAACGGAGGA	80
81	GATTACGAATAAGCAATT ATG GGC AAG CAA AAG CAG CAG ACG ATT TCT CGT TTC GCT CCC	144
1	M G K Q K Q Q T I S R F F A P	15
145	AAA CCC AAA TCC CCG ACT CAC GAA CCG AAT CCG GTA GCC GAA TCA TCA ACA CCG CCA CCG	204
16	K P K S P T H E P N P V A E S S T P P P	35
205	AAG ATA TCC GCC ACT GTA TCC TTC TCT CCT TCC AAG CGT AAG CTT CTC TCC GAC CAC CTC	264
36	K I S A T V S F S P S K R K L L S D H L	55
265	GCC GCC GCG TCA CCC AAA AAG CCT AAA CTT TCT CCT CAC ACT CAA AAC CCA GTA CCC GAT	324
56	A A A S P K K P K L S P H T Q N P V P D	75
325	CCC AAT TTA CAC CAA AGA TTT CTC CAG AGA TTT CTG GAA CCC TCG CCG GAG GAA TAT GTT	384
76	P N L H Q R F L Q R F L E P S P E E Y V	95
385	CCC GAA ACG TCA TCA TCG AGG AAA TAC ACA CCA TTG GAA CAG CAA GTG GTG GAG CTA AAG	444
96	P E T S S S R K Y T P L E Q Q V V E L K	115
445	AGC AAG TAC CCA GAT GTG GTT TTG ATG GTG GAA GTT GGT TAC AGG TAC AGA TTC TTC GGA	504
116	S K Y P D V V L M V E V G Y R Y R F F G	135
505	GAA GAC GCG GAG ATC GCA GCA CGC GTG TTG GGT ATT TAC GCT CAT ATG GAT CAC AAT TTC	564
136	E D A E I A A R V L G I Y A H M D H N F	155
565	ATG ACG GCG AGT GTG CCA ACA TTT CGA TTG AAT TTC CAT GTG AGA AGA CTG GTG AAT GCA	624
156	M T A S V P T F R L N F H V R R L V N A	175

FIG.4A

625	GGA TAC AAG ATT GGT GTA GTG AAG CAG ACT GAA ACT GCA GCC ATT AAG TCC CAT GGT GCA	684
176	G Y K I G V V K Q T E T A A I K S H G A	195
665	AAC CGG ACC GGC CCT TTT TTC CGG GGA CTG TCG GCG TTG TAT ACC AAA GCC ACG CTT GAA	744
196	N R T G P F F R G L S A L Y T K A T L E	215
745	GCG GCT GAG GAT ATA AGT GGT GGT TGT GGT GGT GAA GAA GGT TTT GGT TCA CAG AGT AAT	804
216	A A E D I S G G C G G E E G F G S Q S N	235
805	TTC TTG GTT TGT GTT GTG GAT GAG AGA GTT AAG TCG GAG ACA TTA GGC TGT GGT ATT GAA	864
236	F L V C V V D E R V K S E T L G C G I E	255
865	ATG AGT TTT GAT GTT AGA GTC GGT GTT GTT GGC GTT GAA ATT TCG ACA GGT GAA GTT GTT	924
256	M S F D V R V G V V G V E I S T G E V V	275
925	TAT GAA GAG TTC AAT GAT AAT TTC ATG AGA AGT GGA TTA GAG GCT GTG ATT TTG AGC TTG	9884
276	Y E E F N D N F M R S G L E A V I L S L	295
985	TCA CCA GCT GAG CTG TTG CTT GGC CAG CCT CTT TCA CAA CAA ACT GAG AAG TTT TTG GTG	1044
296	S P A E L L L G Q P L S Q Q T E K F L V	315
1045	GCA CAT GCT GGA CCT ACC TCA AAC GTT CGA GTG GAA CGT GCC TCA CTG GAT TGT TTC AGC	1104
316	A H A G P T S N V R V E R A S L D C F S	335
1105	AAT GGT AAT GCA GTA GAT GAG GTT ATT TCA TTA TGT GAA AAA ATC AGC GCA GGT AAC TTA	1164
336	N G N A V D E V I S L C E K I S A G N L	355
1165	GAA GAT GAT AAA GAA ATG AAG CTG GAG GCT GCT GAA AAA GGA ATG TCT TGC TTG ACA GTT	1224
356	E D D K E M K L E A A E K G M S C L T V	375

FIG.4B

1225	CAT ACA ATT ATG AAC ATG CCA CAT CTG ACT GTT CAA GCC CTC GCC CTA ACG TTT TGC CAT	1284
376	H T I M N M P H L T V Q A L A L T F C H	395
1285	CTC AAA CAG TTT GGA TTT GAA AGG ATC CTT TAC CAA GGG GCC TCA TTT CGC TCT TTG TCA	1344
396	L K Q F G F E R I L Y Q G A S F R S L S	415
1245	AGT AAC ACA GAG ATG ACT CTC TCA GCC AAT ACT CTG CAA CAG TTG GAG GTT GTG AAA AAT	1404
416	S N T E M T L S A N T L Q Q L E V V K N	435
1405	AAT TCA GAT GGA TCG GAA TCT GGC TCC TTA TTC CAT AAT ATG AAT CAC ACA CTT ACA GTA	1464
436	N S D G S E S G S L F H N M N H T L T V	455
1465	TAT GCT TCC AGG CTT CTT AGA CAC TGG GTG ACT CAT CCT CTA TGC GAT AGA AAT TTG ATA	1524
456	Y A S R L L R H W V T H P L C D R N L I	475
1525	TCT GCT CGG CTT GAT GCT GTT TCT GAG ATT TCT GCT TGC ATG GGA TCT CAT AGT TCT TCC	1584
476	S A R L D A V S E I S A C M G S H S S	495
1585	CAG CTC AGC AGT GAG TTG GTT GAA GAA GGT TCT GAG AGA GCA ATT GTA TCA CCT GAG TTT	1644
496	Q L S S E L V E E G S E R A I V S P E F	515
1645	TAT CTC GTG CTC TCC TCA GTC TTG ACA GCT ATG TCT AGA TCA TCT GAT ATT CAA CGT GGA	1704
516	Y L V L S S V L T A M S R S S D I Q R G	535
1705	ATA ACA AGA ATC TTT CAT CGG ACT GCT AAA GCC ACA GAG TTC ATT GCA GTT ATG GAA GCT	1764
536	I T R I F H R T A K A T E F I A V M E A	555
1765	ATT TTA CTT GCG GGG AAG CAA ATT CAG CGG CTT GGC ATA AAG CAA GAC TCT GAA ATG AGG	1824
556	I L L A G K Q I Q R L G I K Q D S E M R	575

FIG.4C

1825	AGT	ATG	CAA	TCT	GCA	ACT	GTG	CGA	TCT	ACT	CTT	TTG	AGA	AAA	TTG	ATT	TCT	GTT	ATT	TCA	1884
576	S	M	Q	S	A	T	V	R	S	T	L	L	R	K	L	I	S	V	I	S	595
1885	TCC	CCT	GTT	GTG	GTT	GAC	AAT	GCC	GGA	AAA	CTT	CTC	TCT	GCC	CTA	AAT	AAG	GAA	GCG	GCT	1944
596	S	P	V	V	V	D	N	A	G	K	L	L	S	A	L	N	K	E	A	A	615
1945	GTT	CGA	GGT	GAC	TTG	CTC	GAC	ATA	CTA	ATC	ACT	TCC	AGC	GAC	CAA	TTT	CCT	GAG	CTT	GCT	2004
616	V	R	G	D	L	L	D	I	L	I	T	S	S	D	Q	F	P	E	L	A	635
2005	GAA	GCT	CGC	CAA	GCA	GTT	TTA	GTC	ATC	AGG	GAA	AAG	CTG	GAT	TCC	TCG	ATA	GCT	TCA	TTT	2064
636	E	A	R	Q	A	V	L	V	I	R	E	K	L	D	S	S	I	A	S	F	655
2065	CGC	AAG	AAG	CTC	GCT	ATT	CGA	AAT	TTG	GAA	TTT	CTT	CAA	GTG	TCG	GGG	ATC	ACA	CAT	TTG	2124
656	R	K	K	L	A	I	R	N	L	E	F	L	Q	V	S	G	I	T	H	L	675
2125	ATA	GAG	CTG	CCC	GTT	GAT	TCC	AAG	GTC	CCT	ATG	AAT	TGG	GTG	AAA	GTA	AAT	AGC	ACC	AAG	2184
676	I	E	L	P	V	D	S	K	V	P	M	N	W	V	K	V	N	S	T	K	695
2185	AAG	ACT	ATT	CGA	TAT	CAT	CCC	CCA	GAA	ATA	GTA	GCT	GGC	TTG	GAT	GAG	CTA	GCT	CTA	GCA	2244
696	K	T	I	R	Y	H	P	P	E	I	V	A	G	L	D	E	L	A	L	A	715
2245	ACT	GAA	CAT	CTT	GCC	ATT	GTG	AAC	CGA	GCT	TCG	TGG	GAT	AGT	TTC	CTC	AAG	AGT	TTC	AGT	2304
716	T	E	H	L	A	I	V	N	R	A	S	W	D	S	F	L	K	S	F	S	735
2305	AGA	TAC	TAC	ACA	GAT	TTT	AAG	GCT	GCC	GTT	CAA	GCT	CTT	GCT	GCA	CTG	GAC	TGT	TTG	CAC	2364
736	R	Y	Y	T	D	F	K	A	A	V	Q	A	L	A	A	L	D	C	L	H	755
2365	TCC	CTT	TCA	ACT	CTA	TCT	AGA	AAC	AAG	AAC	TAT	GTC	CGT	CCC	GAG	TTT	GTG	GAT	GAC	TGT	2424
756	S	L	S	T	L	S	R	N	K	N	Y	V	R	P	E	F	V	D	D	C	775

FIG.4D

2425	GAA CCA GTT GAG ATA AAC ATA CAG TCT GGT CGT CAT CCT GTA CTG GAG ACT ATA TTA CAA	2484
776	E P V E I N I Q S G R H P V L E T I L Q	795
2485	GAT AAC TTC GTC CCA AAT GAC ACA ATT TTG CAT GCA GAA GGG GAA TAT TGC CAA ATT ATC	2544
796	D N F V P N D T I L H A E G E Y C Q I I	815
2545	ACC GGA CCT AAC ATG GGA GGA AAG AGC TGC TAT ATC CGT CAA GTT GCT TTA ATT TCC ATA	2604
816	T G P N M G G K S C Y I R Q V A L I S I	835
2605	ATG GCT CAG GTT GGT TCC TTT GTA CCA GCG TCA TTC GCC AAG CTG CAC GTG CTT GAT GGT	2664
836	M A Q V G S F V P A S F A K L H V L D G	855
2665	GTT TTC ACT CGG ATG GGT GCT TCA GAC AGT ATC CAG CAT GGC AGA AGT ACC TTT CTA GAA	2724
856	V F T R M G A S D S I Q H G R S T F L E	875
2725	GAA TTA AGT GAA GCG TCA CAC ATA ATC AGA ACC TGT TCT TCT CGT TCG CTT GTT ATA TTA	2784
876	E L S E A S H I I R T C S S R S L V I L	985
2785	GAT GAG CTT GGA AGA GGC ACT AGC ACA CAC GAC GGT GTA GCC ATT GCC TAT GCA ACA TTA	2844
896	D E L G R G T S T H D G V A I A Y A T L	915
2845	CAG CAT CTC CTA GCA GAA AAG AGA TGT TTG GTT CTT TTT GTC ACG CAT TAC CCT GAA ATA	2904
916	Q H L L A E K R L V L F V T H Y P E I	935
2905	GCT GAG ATC AGT AAC GGA TTC CCA GGT TCT GTT GGG ACA TAC CAT GTC TCG TAT CTG ACA	2964
936	A E I S N G F P G S V G T Y H V S Y L T	955
2965	TTG CAG AAG GAT AAA GGC AGT TAT GAT CAT GAT GAT GTG ACC TAC CTA TAT AAG CTT GTG	3024
956	L Q K D K G S Y D H D D V T Y L Y K L V	975

FIG.4E

3025	CGT GGT CTT TGC AGC AGG AGC TTT GGT TTT AAG GTT GCT CAG CTT GCC CAG ATA CCT CCA	3084
976	R G L C S R S F G F K V A Q L A Q I P P	995
3085	TCA TGT ATA CGT CGA GCC ATT TCA ATG GCT GCA AAA TTG GAA GCT GAG GTA CGT GCA AGA	3144
996	S C I R R A I S M A A K L E A E V R A R	1015
3145	GAG AGA AAT ACA CGC ATG GGA GAA CCA GAA GGA CAT GAA GAA CCG AGA GGC GCA GAA GAA	3204
1016	E R N T R M G E P E G H E E P R G A E E	1035
3205	TCT ATT TCG GCT CTA GGT GAC TTG TTT GCA GAC CTG AAA TTT GCT CTC TCT GAA GAG GAC	3264
1036	S I S A L G D L F A D L K F A L S E E D	1055
3265	CCT TGG AAA GCA TTC GAG TTT TTA AAG CAT GCT TGG AAG ATT GCT GGC AAA ATC AGA CTA	3324
1056	P W K A F E F L K H A W K I A G K I R L	1075
3325	AAA CCA ACT TGT TCA TTT TGA TTAACTTTAACAATTATAGCAACTGCAAGGCTTGATCATCTGTTAGTTGCG	3397
1076	K P T C S F *	1082
3398	TACTACTT ATG TGT ATT AGT ATA ACA AGA AAA GAG AAT TAG AGAG ATG GAT TCT AAT CCG	3458
1	M C I S I T R K E N * M D S N P	5
3459	GTG TTG CAG TAC ATC TTT TCT CCA CCC GCA TAA AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	3522
6	V L Q Y I F S P P A *	16

FIG.4F

MSH3-At	--MGKOK-----	QOTISRFFAPKPKSp- THE -PNPVAESSTPPK-----	ISATVSFSPSKRLL
MSH3-Sc	MVIGNEPKLVLLRAKSSANRFILLNLLTIMAGOPTISRF FKAVKSEL THKQEQEVAVNGAGSESICLDTEEDNLSVASSTVTNDSFPLKGS		
MSH3-At	SDHLAASP KPKLSPH IQNPVPDPNLHQRFLEP-----	SPEEYMPETSS--SRKYTPLEQQVVELKSKYPDVL MEVGYR RF	
MSH3-Sc	VSSKNSK SEKTS GTSTIFNDIDFAKKLDRIMK RSD ENVEAEDEEEGEE DFVKKK ARKSP TAKL TPLDKQVKDLKM HRD KVLVIRVGYKYKC		
MSH3-At	EGEDAEIAARV LGI YAH-----MDHN-----	FMTASVPTFRLN FHVRRL VNAGYKIGV KQ TE TA AIKSH--GANRTGP FFRGL SALYTKA	
MSH3-Sc	FAEDAVTVSRIL HLIKL VP PKL TIDESNPQDCNHRQ EAYCS FPDVRLNVHLERLVHHNLKVAVE EQ AE TS AIKK HD PGASKSSV EEK ISNVFTKA		
MSH3-At	ILEAAEDISGGCGGEGEG FG SQSNFLVCVDERVKSET LG CGIEMSFDVRVG VE ISTGEV VEE FN DN -N FM RSQ LE AV IL SL SPA ELL LG -QP		
MSH3-Sc	IFGVNSTFVLR-----GKR-----	ILGDTNSIWALSRDVHQGVAKYSLISVNLNGEV YDE FE EP N LA DEK LQIRIKYLQPI EVLVNTDD	
MSH3-At	LSQOTE KFL VAMAGPTSNVRVERASLD CF SNGNA VD EV IS LCEKISAGNLED DK EMK LE AEKGMSCLTVHTIMN PH LTVQALALTF CH LKQFG		
MSH3-Sc	LPLHVAK FF KDIS CP L HK Q EY DL ED HVQA IK V NE K IQ LSPSL-----	IRLVSKLYSHMEYN	
MSH3-At	FERILYOGASFRSL S NTE MT L S ANT L Q Q LEVVKNSD GE SE GS L F HNMN HT L IV GSRL RH W TH P L CD R N L ISAR LD AV SE ISACMGSHSS		
MSH3-Sc	NEQV ML IP S IY SP FA SK I HM LLDP NS LS Q SLDI FT HD--G GK -G SL F WL LD H IR IS F GL RM L RE IL K PL VDV HQ IEER LD AI EC IT SE INNS...		
MSH3-At	QLSSELVEEGSERAI VS PEFYLVLS SV L T AMSRSSD IQ R IG IT RI F HR I AK ATE FI AV ME AILLAGKQ IQ RLG IK QDSEMR S MQS-ATVR ST LL RK		
MSH3-Sc	-----IFFESLNQMLN HT P DL LR LN RI MY GI TS R KE Y Y FLKQ IT S F VD HF K M HQSYLSE HF KSSDGRIGK Q SP L FR		
MSH3-At	LISV ISS PPVVDNAG KL SAL N KEA AV RG...DL LD IL ITS -SD Q PE LA EARQAVLVIRE KL DSSIAS FR KK L AI R N LE FL OV SG IT HL IE LP		
MSH3-Sc	L FS ELNELLST Q L PH FL TM IN VS AV ME KNSDKQ VM DF FN LN NY DC SE GI IK IQ RE SESV RS Q L KEELAE IR K YL K RP YL N FRDEVDYL IE VKNS		

FIG. 5A

MSH3-At	VDSKVP[PHNMW]KVNSTKKTIRYHPPEIVAGLDELALATEHLAIVNRASWDSFLKSFSRYTIDFKAAVQALALDCLHSLSTLSRNKNYVRPEFVDD
MSH3-Sc	QIKDLPDDMIKVNNTKMWSRFTTPRTQKLTKLEYKDLIRESELOYKEFLNKITAETELRKITLNLAOYDCILSLAATSCNWNVVRPTFVNG
MSH3-At	CEPVEINIQSGRHPVLETILQDNFVPNDTILHAEGEYCOIITGPNMGKSCYIROVALISIMAOVGSFVPASFAKLHVLGDVFTRMGASDSIQHG
MSH3-Sc	QQ--AIIAKNARNPIIES-LDVHYVPNDIMSPENGKINIITGPNMGKSSYIROVALTIMAQIGSFVPAEEIRLSIFENVLTRIGAHDIDIING
MSH3-At	RSTFLEELSEASHIIRTCSRSRLVILDELGRGISTHDGVAIAVATLQHLLAEKRC-LVLFVTHYPEIAEISNGFPGSVGTYHVSYLTLQKDKGSY
MSH3-Sc	DSTFKVEMLDILHILKNCNKRSLLLDDEVGRGIGTHDGAISYALIKYFSELSDCPLILFTTHFPMIGEIKS--PLIRNYHMDYVEEQK--TGE
MSH3-At	DHDDVTYLYKLVRGLCSRSFGFKVAQLAQIPPSCIIRRAISMAKLEAEVRARERNTRMGEPEGHEEPRGAEESISALGDLFADLKFAISEEDPWK
MSH3-Sc	DMMSVIFLYKLKGLTYSYGMNVAKLARLDKDIINRAFSISEELRKESIN-----EDALKL--FSSLRILKSDN---
MSH3-At	AFFFLKHAWKIAGKIRLKPTCSF---
MSH3-Sc	-----ITATDKLAKLLSLDIH

FIG.5B

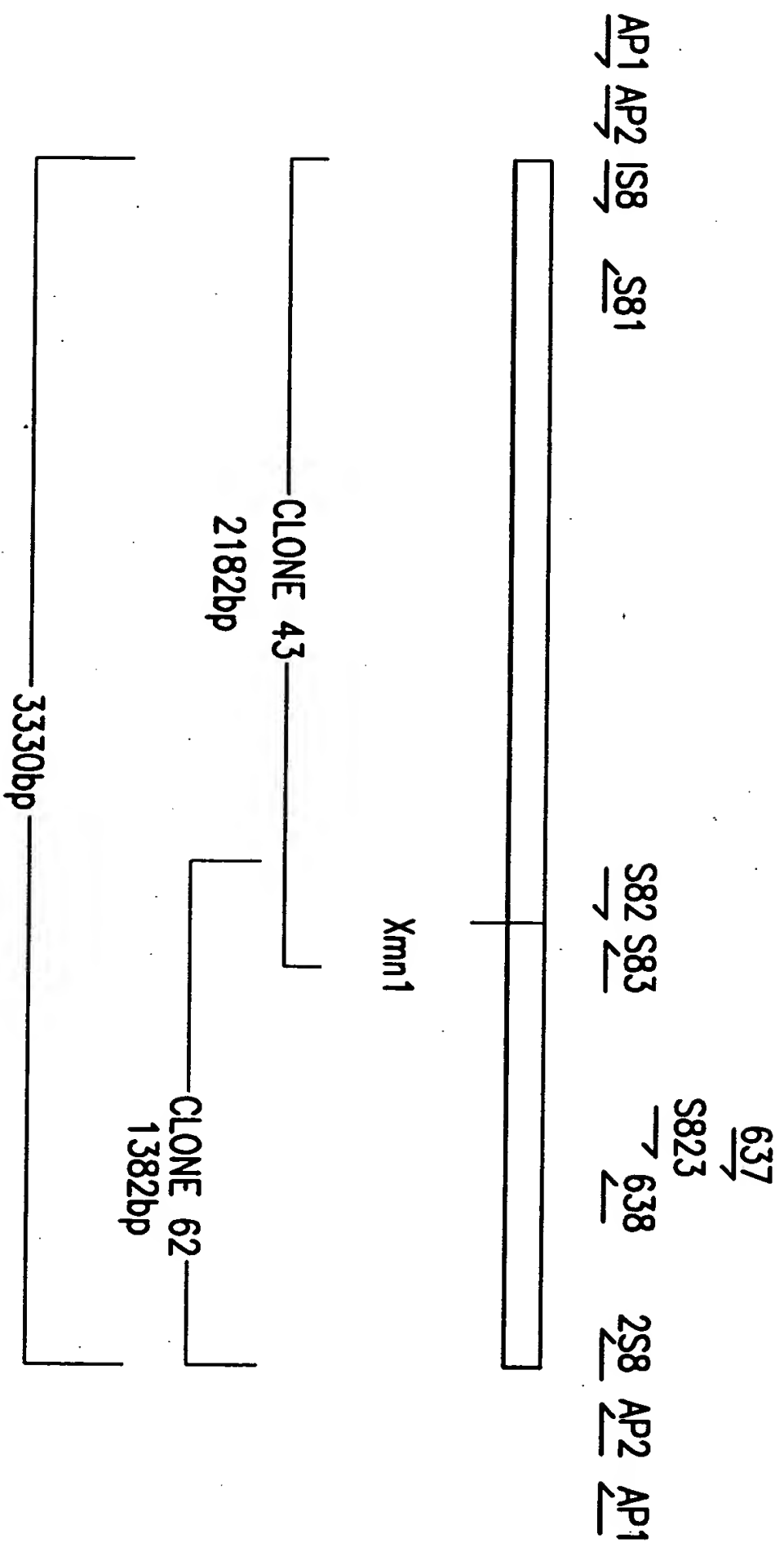
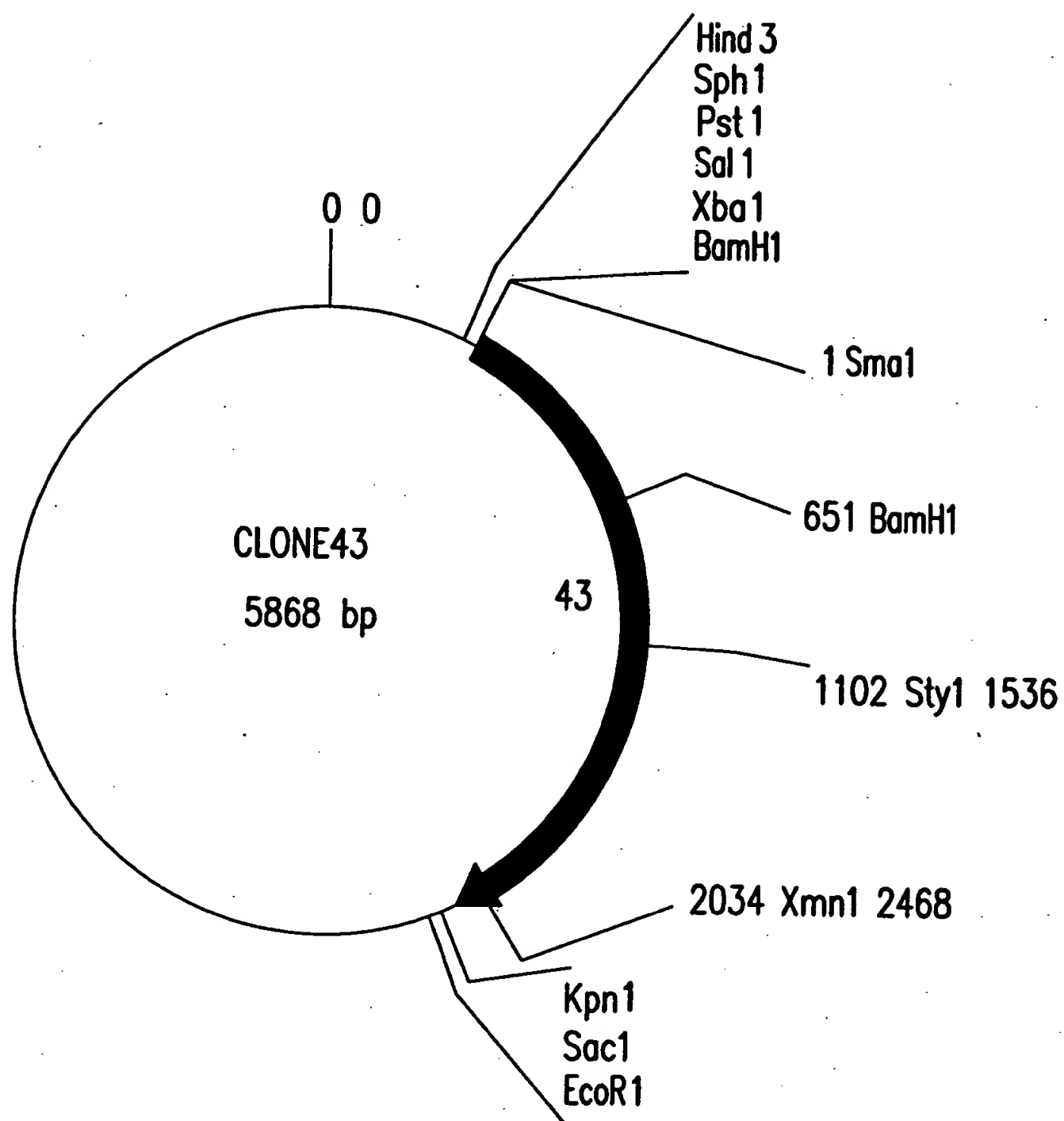
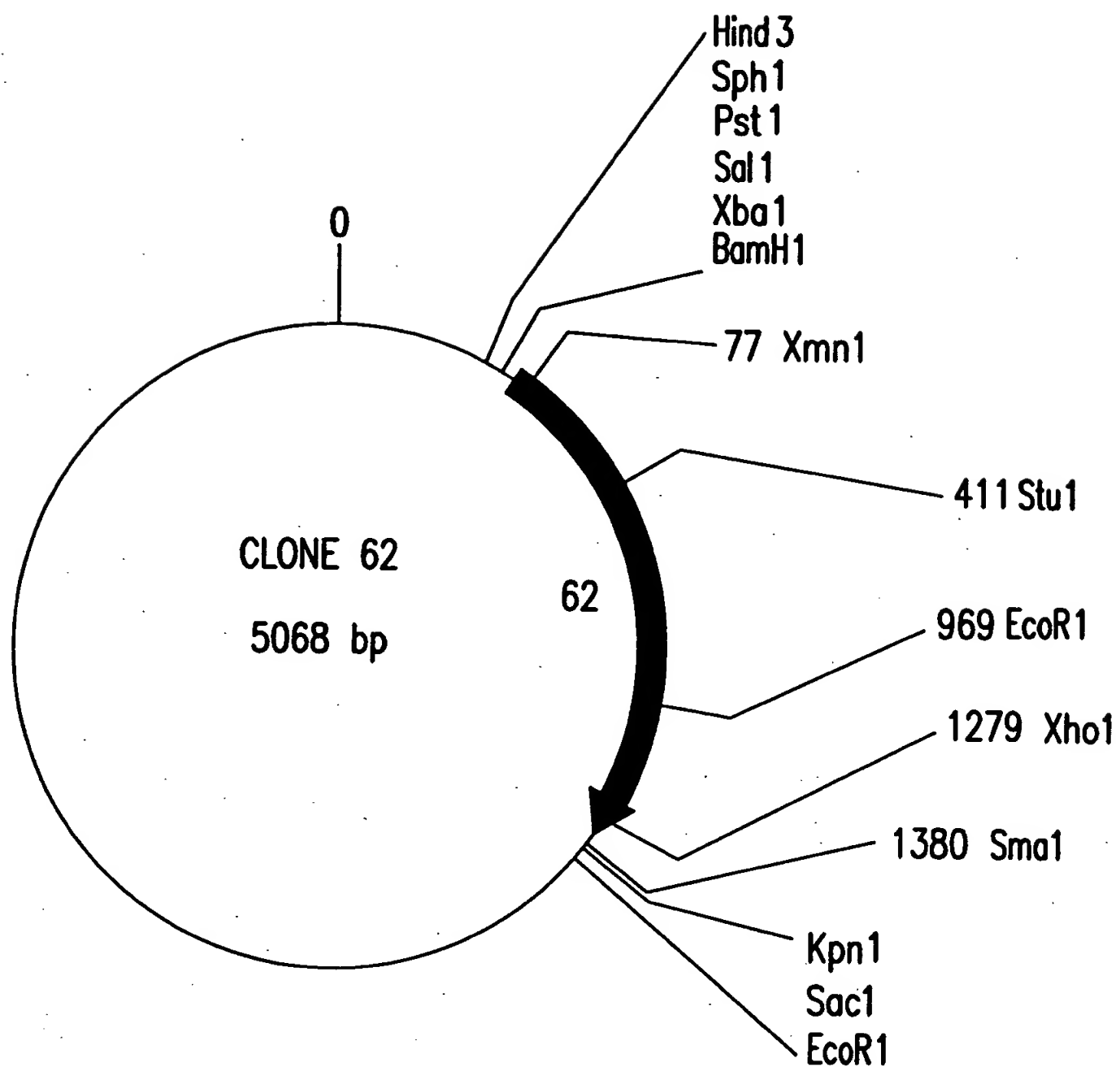


FIG.6



COMMENTS/REFERENCES: 43=5' SIDE OF S8 (AtMSH6) 2182bp IN pUC18/Sma1

FIG.7



COMMENTS/REFERENCES: 62=3' SIDE OF S8 (AtMSH6) 1379bp IN pUC18/Sma1

FIG.8

1	AAAAGTTGAGCCCTGAGGAGTATCGTTCCGCCAATTCTACGACGCAAGCGGAAATTTTGGCGCCAATCTTCCCCC	80
81	TTTCGAATTCTCTCAGCTCAAAACATCGTTTCTCTCTCACTCTCTCACAATTCAAAA	153
1		M Q R Q 4
154	AGA TCG ATT TTG TCT TTC TTT CAA AAA CCC ACC GCG GCG ACT ACG AAG GGT TTG GTT TCC	213
5	R S I L S F F Q K P T A A T T K G L V S	24
214	GGC GAT GCT GCT AGC GGC GGC GGC AGC GGA GGA CCA CGA TTT AAT GTG AAG GAA GGG	273
25	G D A A S G G G S G G P R F N V R E G	44
274	GAT GCT AAA GGC GAC GCT TCT GTA CGT TTT GCT GTT TCG AAA TCT GTC GAT GAG GTT AGA	333
45	D A K G D A S V R F A V S K S V D E V R	64
334	GGA ACG GAT ACT CCA CCG GAG AAG GTT CCG CGT CGT GTC CTG CCG TCT GGA TTT AAG CCG	393
65	G T D T P P E K V P R R V L P S G F K P	84
394	GCT GAA TCC GCC GST GAT GCT TCG TCC CTG TTC TCC AAT ATT ATG CAT AAG TTT GTA AAA	453
85	A E S A G D A S S L F S N I M H K F V K	104
454	GTC GAT GAT CGA GAT TGT TCT GGA GAG AGG AGC CGA GAA GAT GTT GTT CCG CTG AAT GAT	513
105	V D D R D C S G E R S R E D V V P L N D	124
514	TCA TCT CTA TGT ATG AAG GCT AAT GAT GTT ATT CCT CAA TTT CGT TCC AAT AAT GGT AAA	573
125	S S L C M K A N D V I P Q F R S N N G K	144
574	ACT CAA GAA AGA AAC CAT GCT TTT AGT TTC AGT GGG AGA GCT GAA CTT AGA TCA GTA GAA	633
145	T Q E R N H A F S F S G R A E L R S V E	164
634	GAT ATA GGA GTA GAT GGC GAT GTT CCT GGT CCA GAA ACA CCA GGG ATG CGT CCA CGT GCT	693
165	D I G V D G D V P G P E T P G M R P R A	184

FIG. 9A

694	TCT CGC TTG AAG CGA GTT CTG GAG GAT GAA ATG ACT TTT AAG GAG GAT AAG GTT CCT GTA	753
185	S R L K R V L E D E M T F K E D K V P V	204
754	TTG GAC TCT AAC AAA AGG CTG AAA ATG CTC CAG GAT CCG GTT TGT GGA GAG AAG AAA GAA	813
205	L D S N K R L K M L Q D P V C G E K K E	224
814	GTA AAC GAA GGA ACC AAA TTT GAA TGG CTT GAG TCT TCT CGA ATC AGG GAT GCC AAT AGA	873
225	V N E G T K F E W L E S S R I R D A N R	224
874	AGA CGT CCT GAT GAT CCC CTT TAC GAT AGA AAG ACC TTA CAC ATA CCA CCT GAT GTT TTC	933
245	R R P D D P L Y D R K T L H I P P D V F	264
934	AAG AAA ATG TCT GCA TCA CAA AAG CAA TAT TGG AGT GTT AAG AGT GAA TAT ATG GAC ATT	993
265	K K M S A S Q K Q Y W S V K S E Y M D I	284
996	GTG CTT TTC TTT AAA GTG GGG AAA TTT TAT GAG CTG TAT GAG CTA GAT GCG GAA TTA GGT	1053
285	V L F F K V G K F Y E L Y E L D A E L G	304
1054	CAC AAG GAG CTT GAC TGG AAG ATG ACC ATG AGT GGT GTG GGA AAA TGC AGA CAG GTT GGT	1113
305	H K E L D W K M T M S G V G K C R Q V G	324
1114	ATC TCT GAA AGT GGG ATA GAT GAG GCA GTG CAA AAG CTA TTA GCT CGT GGA TAT AAA GTT	1173
325	I S E S G I D E A V Q K L L A R G Y K V	344
1174	GGA CGA ATC GAG CAG CTA GAA ACA TCT GAC CAA GCA AAA GCC AGA GGT GCT AAT ACT ATA	1233
345	G R I E Q L E T S D Q A K A R G A N T I	364
1234	ATT CCA AGG AAG CTA GTT CAG GTA TTA ACT CCA TCA ACA GCA AGC GAG GGA AAC ATC GGG	1293
365	I P R K L V Q V L T P S T A S E G N I G	384
1294	CCT GAT GCC GTC CAT CTT CTT GCT ATA AAA GAG ATC AAA ATG GAG CTA CAA AAG TGT TCA	1353
385	P D A V H L L A I K E I K M E L Q K C S	404

FIG.9B

1354	ACT	GTG	TAT	GGA	TTT	GCT	TTT	GTT	GAC	TGT	GCT	GCC	TTG	AGG	TTT	TGG	GTT	GGG	TCC	ATC	1413
405	T	V	Y	G	F	A	F	V	D	C	A	A	L	R	F	W	V	G	S	I	424
1414	AGC	GAT	GAT	GCA	TCA	TGT	GCT	GCT	CTT	GGA	GCG	TTA	TTG	ATG	CAG	GTT	TCT	CCA	AAG	GAA	1473
425	S	D	D	A	S	C	A	A	L	G	A	L	L	M	Q	V	S	P	K	E	444
1474	GTG	TTA	TAT	GAC	AGT	AAA	GGG	CTA	TCA	AGA	GAA	GCA	CAA	AAG	GCT	CTA	AGG	AAA	TAT	ACG	1533
445	V	L	Y	D	S	K	G	L	S	R	E	A	Q	K	A	L	R	K	Y	T	464
1534	TTG	ACA	GGG	TCT	ACG	GCG	GTA	CAG	TTG	GCT	CCA	GTA	CCA	CAA	GTA	ATG	GGG	GAT	ACA	GAT	1593
465	L	T	G	S	T	A	V	Q	L	A	P	V	P	Q	V	M	G	D	T	D	484
1594	GCT	GCT	GGA	GTT	AGA	AAT	ATA	GAA	TCT	AAC	GGA	TAC	TTT	AAA	GGT	TCT	TCT	GAA	TCA		1653
485	A	A	G	V	R	N	I	I	E	S	N	G	Y	F	K	G	S	S	E	S	504
1654	TGG	AAC	TGT	GCT	GTT	GAT	GGT	CTA	AAT	GAA	TGT	GAT	GTT	GCC	CTT	AGT	GCT	CTT	GGA	GAG	1713
505	W	N	C	A	V	D	G	L	N	E	C	D	V	A	L	S	A	L	G	E	524
1714	CTA	ATT	AAT	CAI	CTG	TCT	AGG	CTA	AAG	CTA	GAA	GAT	GTA	CTT	AAG	CAT	GGG	GAT	ATT	TTT	1773
525	L	I	N	H	L	S	R	L	K	L	E	D	V	L	K	H	G	D	I	F	544
1774	CCA	TAC	CAA	GTT	TAC	AGG	GGT	TGT	CTC	AGA	ATT	GAT	GGC	CAG	ACG	ATG	GTA	AAT	CTT	GAG	1833
545	P	Y	Q	V	Y	R	G	C	L	R	I	D	G	Q	T	M	V	N	L	E	564
1834	ATA	TTT	AAC	AAT	AGC	TGT	GAT	GGT	GGT	CCT	TCA	GGG	ACC	TTG	TAC	AAA	TAT	CTT	GAT	AAC	1893
565	I	F	N	N	S	C	D	G	G	P	S	G	T	L	Y	K	Y	L	D	N	584
1894	TGT	GTT	AGT	CCA	ACT	GGT	AAG	CGA	CTC	TTA	AGG	AAT	TGG	ATC	TGC	CAT	CCA	CTC	AAA	GAT	1953
585	C	V	S	P	T	G	K	R	L	L	R	N	W	I	C	H	P	L	K	D	604
1954	GTA	GAA	AGC	ATC	AAT	AAA	CGG	CTT	GAT	GTA	GTT	GAA	GAA	TTC	ACG	GCA	AAC	TCA	GAA	AGT	2013
605	V	E	S	I	N	K	R	L	D	V	V	E	E	F	T	A	N	S	E	S	624

FIG.9C

2014	ATG CAA ATC ACT GGC CAG TAT CTC CAC AAA CTT CCA GAC TTA GAA AGA CTG CTC GGA CGC	2073
625	M Q I T G Q Y L H K L P D L E R L L G R	644
2074	ATC AAG TCT AGC GTT CGA TCA TCA GCC TCT GTG TTG CCT GCT CTT CTG GGG AAA AAA GTG	2133
645	I K S S V R S S A S V L P A L L G K K V	664
2134	CTG AAA CAA CGA GTT AAA GCA TTT GGG CAA ATT GTG AAA GGG TTC AGA AGT GGA ATT GAT	2193
665	L K Q R V K A F G Q I V K G F R S G I D	684
2194	CTG TTG TTG GCT CTA CAG AAG GAA TCA AAT ATG ATG AGT TTG CTT TAT AAA CTC TGT AAA	2253
685	L L L A L Q K E S N M M S L L Y K L C K	704
2254	CTT CCT ATA TTA GTA GGA AAA AGC GGG CTA GAG TTA TTT CTT TCT CAA TTC GAA GCA GCC	2313
705	L P I L V G K S G L E L F L S Q F E A A	724
2314	ATA GAT AGC GAC TTT CCA AAT TAT CAG AAC CAA GAT GTG ACA GAT GAA AAC GCT GAA ACT	2373
725	I D S D F P N Y Q N Q D V T D E N A E T	744
2374	CTC ACA ATA CTT ATC GAA CTT TTT ATC GAA AGA GCA ACT CAA TGG TCT GAG GTC ATT CAC	2433
745	L T I L I E L F I E R A T Q W S E V I H	764
2434	ACC ATA AGC TGC CTA GAT GTC CTG AGA TCT TTT GCA ATC GCA GCA AGT CTC TCT GCT GGA	2493
765	T I S C L D V L R S F A I A A S L S A G	784
2494	AGC ATG GCC AGG CCT GTT ATT TTT CCC GAA TCA GAA GCT ACA GAT CAG AAT CAG AAA ACA	2553
785	S M A R P V I F P E S E A T D Q N Q K T	804
2554	AAA GGG CCA ATA CTT AAA ATC CAA GGA CTA TGG CAT CCA TTT GCA GTT GCA GCC GAT GGT	2613
805	K G P I L K I Q G L W H P F A V A A D G	824
2614	CAA TTG CCT GTT CCG AAT GAT ATA CTC CTT GGC GAG GCT AGA AGA AGC AGT GGC AGC ATT	2673
825	Q L P P V P N D I L L L G E A R R S S G S I	844

FIG.9D

2674	CAT CCT CGG TCA TTG TTA CTG ACG GGA CCA AAC ATG GGC GGA AAA TCA ACT CTT CTT CGT	2733
845	H P R S L L L T G P N M G G K S T L L R	864
2734	GCA ACA TGT CTG GCC GTT ATC TTT GCC CAA CTT GGC TGC TAC GTG CCG TGT GAG TCT TGC	2793
865	A T C L A V I F A Q L G C Y V P C E S C	884
2794	GAA ATC TCC CTC GTG GAT ACT ATC TTC ACA AGG CTT GGC GCA TCT GAT AGA ATC ATG ACA	2853
885	E I S L V D T I F T R L G A S D R I M T	904
2854	GGA GAG AGT ACC TTT TTG GTA GAA TGC ACT GAG ACA GCG TCA GTT CTT CAG AAT GCA ACT	2913
905	G E S T F L V E C T E T A S V L Q N A T	924
2914	CAG GAT TCA CTA GTA ATC CTT GAC GAA CTG GGC AGA GGA ACT AGT ACT TTC GAT GGA TAC	2973
925	Q D S L V I L D E L G R G T S T F D G Y	944
2974	GCC ATT GCA TAC TCG GTT TTT CGT CAC CTG GTA GAG AAA GTT CAA TGT CGG ATG CTC TTT	3033
945	A I A Y S V F R H L V E K V Q C R M L F	964
3034	GCA ACA CAT TAC CAC CCT CTC ACC AAG GAA TTC GCG TCT CAC CCA CGT GTC ACC TCG AAA	3093
965	A T H Y H P L T K E F A S H P R V T S K	984
3094	CAC ATG GCT TGC GCA TTC AAA TCA AGA TCT GAT TAT CAA CCA CGT GGT TGT GAT CAA GAC	3153
985	H M A C A F K S R S D Y Q P R G C D Q D	1004
3154	CTA GTG TTC TTG TAC CGT TTA ACC GAG GGA GCT TGT CCT GAG AGC TAC GGA CTT CAA GTG	3213
1005	L V F L Y R L T E G A C P E S Y G L Q V	1024
3214	GCA CTC ATG GCT GGA ATA CCA AAC CAA GTG GTT GAA ACA GCA TCA GGT GCT GCT CAA GCC	3273
1025	A L M A G I P N Q V V E T A S G A A Q A	1044
3274	ATG AAG AGA TCA ATT GGG GGA AAC TTC AAG TCA AGT GAG CTA AGA TCT GAG TTC TCA AGT	3333
1045	M K R S I G E N F K S S E L R S E F S S	1064

FIG.9E

3334	CTG	CAT	GAA	GAC	TGG	CTC	AAG	TCA	TTG	GTG	GGT	ATT	TCT	CGA	GTC	GCC	CAC	AAC	AAT	GCC	3393
1065	L	H	E	D	W	L	K	S	L	V	G	I	S	R	V	A	H	N	N	A	1084
3394	CCC	ATT	GGC	GAA	GAT	GAC	TAC	GAC	ACT	TTG	TTT	TGC	TTA	TGG	CAT	GAG	ATC	AAA	TCC	TCT	3453
1085	P	I	G	E	D	D	Y	D	T	L	F	C	L	W	H	E	I	K	S	S	1104
3454	TAC	TGT	GTT	CCC	AAA	TAA	ATG	GCT	ATG	ACA	TAA	CAC	TAT	CTGA	AGCT	CGTTA	AGTCT	TTG	CC	CTCT	3521
1105	Y	C	V	P	K	*	M	A	M	T	*									5	
3522	G	ATG	TTT	ATT	CCT	CTT	AAA	AAA	TGC	TTA	TAT	ATC	AAA	AAA	TTG	TTT	CCT	CGA	TTA	AAA	3579
1	M	F	I	P	L	K	K	C	L	Y	I	K	K	L	F	P	R	L	K		19
3580	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	3606
20	K	K	K	K	K	K	K	K	K	K	K	K	K	K	K	K	K	K	K	28	

FIG.9F

AtMSH6-miMOR...QRSLSF.....QKPTAATTKGLVSGDASGG- GGSGPRFNVREGDAKGDASVRFVSKSVDEVRGTD
MSH6_ yeast	MAPATPKTSTAHEENGSTSSQKKMKQSSLSFESKQVPSGTPSKVQKPTPAILENTATDKITKNPQGGKTGKLFVDVEDND-LTIAEETVSTVRSDIMHSQE
AtMSH6-mi	PPEKVPRRVLPSGFKPAESAGDASSLF SNIMHK...-FVKVDDRD...-CSGERSREDVPLN- DSSLCKM ANDVIPQFRSNGKTQERNHAFSFSG- RAELRS
MSH6_ yeast	POS DTMLNSNTEPKSTTDEDLSSQSRNHKRRVNYAESDDDDSDDTFTAKRKKGKVVDESEDEYLPDKNDGEDEDDIADDKEDIKGELAEDSGDDDDLIS
AtMSH6-mi	VEDIGVDGVPGETPGMRPRASRLKRVLEDEMTFKEDKVPVLDSNKRKLMLQDPVCGEKKKEVNEGTFEML ESSRIRDANRRRPDDPL YDRKTLHIPDVFKM
MSH6_ yeast	LAETTSKKKFSYNTSHSSSPFTRNISRDNSKKKSRRPNQAPSRSYNPSSHQPSATSSSKFNKONEERYQWLVE-- RDAQRRPKSDPEYDPR TLYIPSSAWNK
AtMSH6-mi	SASQKQYWSVKS SEYMDIVLFFKVGFYELYELDAELGHKELDWKMTMSGVGKCRQVGISESGIDEAVOKLLARGKYVGRIEQL ETS DOAKAR- GANTI IIPRKL VQ
MSH6_ yeast	TPFEKQYWEIKSK MWD CIV FFKKGGFFELYEKDALLANALFDLKIAGGGRANMQLGIP EMS FYWAQFIOMGYKVAKVDO RES MLAKEMREGSKGIVKREL QC
AtMSH6-mi	VLTPSI ASEGNIGP-- DAVHL LAIKE...-IKMELOKS...-TVYGF AFV DC AAL RFWGSISDD ASC AL GAL LMQVSPKEVL YDS KG LS REAOKALR
MSH6_ yeast	ILIS GILTDGMLHSD LAT FC LAI REEPGNFY NET QLD SS TI VOK LNTK IF GA FID IT AT GELQMLEFED SECT KLDT MSQ VR MEV MERNN ST LANKIVK
AtMSH6-mi	KYTLTGSTAVQLAPVPQVMGDT DA AGVRN IT ESNGYFKGSSES WNC AVDGLNEC-- DVAL SAL GEL INHL SRL KLED...-VLKHGDIFPYQVYRGCLRIDGQIMV
MSH6_ yeast	FNSAPNAIFNEVKAGEEFY-- DCDK TYAE II SSSEYFS TEED PEVLKSYDTGKKVGFSA FG LLY LKML KL DKNL ISM KN IKEYDFVKSQHS MVL DG IT LQ
AtMSH6-mi	NLEIF NNS CD GGPSGTL YK YLDNCV SP TGKRLRN WIC HP LK DVEST INK R LDV EEFTANSESMQITGOYL HKLP DLER LL GR IKS
MSH6_ yeast	NLEIF SNS FD GS DK GT LF KL FN RAIT PM GKRM KKML HP LR KND IES R LD SV DSL LODIT LR EQLEIT FS KL PD LER ML AR HS RTIKVKDFEKVITAFETII
AtMSH6-mi	----SVRSS-----ASVLP ALL GKKVLKOR VKA FGQIVKGFRSGID LL LALQKE-----SNM SSL YKLCKLP IL VGKSG LE LF LSQ FEAA
MSH6_ yeast	ELQD SL KNNDLKGDVSKYISS FP EGLVE AV KSWTNA FER OKAINENI IV PO RG FD IE FDK SM DR IQ ELEDELM ET ILTYRKQ FK CSN IQ YKDSG KEI Y VT IEIPIS
AtMSH6-mi	IDSD FP N-----YQ NO D-----VT D EN AET LT IL IE L FIERATQ-----WSEV HT IS IC LD VL RSFA IA ASLSAGSM RPV IF PE SEATDQ N
MSH6_ yeast	ATKN VP SN WQ MAANKTYKR YV SD EV RALARSMA EAK E IHK TL EE DL KN RL CQ K DA HYNT IM PT IQ AIS NI D CL LAIT RT SEYLGAP SC RPT IV DEVDSK TNT

FIG. 10A

AtMSH6-mi	OKTKGPILKIQGLWHPFA--VAADGQLPVNDILLGEARRSSGSIHPRSLLLTGPNMGGKSTILLRATCLAVIFAQLGCYVPCESCEISLVDITFTIRLGASDRIMT
MSH6_yeast	QLNG--FLKFKSLRHPCFNLGATTAKDFIPNDIELGKEQ-----PRLLGLTGANNAAGKSTILLRMACIAVIMAQMGCVPCESAVLTPIDRIMTRLGANDNIMQ
AtMSH6-mi	GESTFLVECTEIASVLQONATQDSLVLDELGRGISTFDGYAIAYSVFRHLVEKVQCRMFLFATHYHPLTKEFFASHPRVTSKHIMACAFKSRSDYQPRGCDQDLVFLY
MSH6_yeast	GKSTFFVELAETKKILLDMATNRSLLVDELGRGSSSDGFATAESVLHHVATHIIQSLGFATHYGTILASSFKHHPQVRPLKMSILVDEAT-----RNVTFLY
AtMSH6-mi	RLTEGACPESYGLQVALMAGIPNOVETASGAQ-----AMKRSIGENFKSSSELRSSEFSSLHEDWLKSLVGISRVAHNNAPIGE---DDYDTLFLCLWHEIK
MSH6_yeast	KMLEGQSEGSGFGMHVASMCGISKEIIDNAQIAADNLEHTSRLVKERDLAANNLNGEIVSVPGGLQSDFVRIAYGDG-LKNTKLGSGEGLNNDMNIRNVLKSLF
AtMSH6-mi	SSYCVPK-
MSH6_yeast	SIIDDLQS

FIG. 10B

TTTTTTGGTTGCTAACAATAAAGGTATACGGTTTTATGTCATCAATATAA	50
CTATATATAAAAGAAATGAAAGATATATATTGTTTTTTCATTTATCAAAC	100
AAAACAACAAGACTTTTTTTTTTACTTTTTTACATTGGTCAACAAAATACAA	150
GATAAACGACATCGTTTAATCATTTCCCAATTTTACCCCTAAGTTTAACA	200
CCTAGAACCCTTCTCCATCTTCGCAAGCACAGCCTGATTAGGAACAGCTTT	250
ACCATTCATATTCTGAACTACCTGAGTCCTCTCATTGATCTGTTTCG	300
CCAAATCCGCTTGTGACATCTTCTTCTCCAATCTCGCTTTCTGTATCATC	350
AACCTCACCTCTGCTTTTACACGATCCATCGCCGAGGCTCTGTTTCTTC	400
TTCCAGCTTCTTCGTGTTAATCACCGGAACCGCCGTAGATTTCCCCTTTT	450
TGTTTGAACCGGCATCGAATTTCTTAACCGTTTGAACCGCGACACCGTTT	500
CTCAGAGCTGCGTTAACCGCTTTCTGGATCGCGTAGGTCTTGGCTCTTTTG	550
TTTTGATTTGTGGAGAACTACTGGTTCCTAGTCTTGTGTTACTGCTCCTG	600
GGTATCTGCTCGGCATCGTCGATGAATTGAGAGAAAGGAACAACGCGAAA	650
ATTTTATTAATCTGAGTTTTTGAATTTGAGAAACGATGAAGATGAAGAATG	700
TTGTTGAGAGGATTGTGATATTTATATATACGAAGATTGGTTTCTGGAGA	750
ATTCGATCATCTTTTTCTCCATTTTCTGCTCTGGAACGTTCTTAGAGATG	800
ATTGACGACGTGTCATTATCTGATTTGCAGTTAACCAATGCTTTTTGGGT	850
TGGATTCGTGGTACACCATATTATCCGATTTGGCTCAATGGTTTTATATA	900
AATTTGGTTTTCGGTTCTGGTTATGAGTTATCATTAAAATTAAGCTAACCA	950
AAAATTTTCGTAAAATTTATTTCTGGTTTCAATTCGGATCCCTTACTTCCA	1000
GAACCGAATTATTCGAAACCGGGGTTAGCCGAACCGAATACCAATGCCTG	1050
ATTGACTCGTTGGCTAGAAAGATCCAACGGTATACAATAATAGAACATAA	1100
ATCGGACGGTCATCAAAGCCTCAAAGAGTGAACAGTCAACAAAAAAAGTT	1150
GAGCCCTGAGGAGTATCGTTTTCCGCCATTTCTACGACGCAAGGCGAAAAT	1200
TTTTGGCGCCAATCTTTCCCCCTTTTGAATTCTCTCAGCTCAAAACATC	1250
GTTTCTCTCTCACTCTCTCTCACAATTCAAAAAATGCAGCGCCAGAGAT	1300
CGATTTTGTCTTTCTTCCAAAAACCCACGGCGGGCGACTACGAAGGGTTTG	1350
GTTTCCGGCGATGCTGCTAGCGGCGGGGGCGGCAGCGGAGACCACGATTT	1400
AATGTGAAGGAAGGGGATGCTAAAGGCGACGCTTCTGTACGTTTTGCTGT	1450
TTCGAAATCTGTGATGAGGTTAGAGGAACGGATACTCCACCGGAGAAGG	1500
TTCCGCGTCGTGTCCTGCCGTCTGGATTTAAGCCGGCTGAATCCGCCGGT	1550
GATGCTTCGTCCCTGTTCTCCAATATTATGCATAAGTTTGTAAGTTCGA	1600
TGATCGAGATTGTTCTGGAGAGAGGTACTAATCTTCGATTCTCTTAATTT	1650
TGTTATCTTTAGCTGGAAGAAGAAGATTCTGTGAATTTGTTGTATTCGTT	1700
GGAGAGATTCTGATTACTGCATTGGATCGTTGTTTACAAATTTTCAGGAG	1750
CCGAGAAGATGTTGTTCCGCTGAATGATTCATCTCTATGTATGAAGGCTA	1800
ATGATGTTATTCCTCAATTTCTGTTCCAATAATGGTAAACTCAAGAAAGA	1850
AACCATGCTTTTAGTTTCAGTGGGAGAGCTGAACTTAGATCAGTAGAAGA	1900
TATAGGAGTAGATGGCGATGTTCTGGTCCAGAAACACCAGGGATGCGTC	1950
CACGTGCTTCTCGCTTGAAGCGAGTTCTGGAGGATGAAATGACTTTTAAG	2000
GAGGATAAGGTTCTGTATTGGACTCTAACAAAAGGCTGAAAATGCTCCA	2050

FIG. 11A

GGATCCGGTTTGTGGAGAGAAGAAAGAAGTAAACGAAGGAACCAAATTTG	2100
AATGGCTTGAGTCTTCTCGAATCAGGGATGCCAATAGAAGACGTCCTGAT	2150
GATCCCCCTTACGATAGAAAGACCTTACACATACCACCTGATGTTTTCAA	2200
GAAAATGTCTGCATCACAAAAGCAATATTGGAGTGTTAAGAGTGAATATA	2250
TGGACATTGTGCTTTTCTTTAAAGTGGTTAGTAACTATTAATCTAGTGTT	2300
CAATCCATTTCTCAATGTGATTTGTTCACTTACATCTGTTTACGTTATG	2350
CTCTTCTCAGGGGAAATTTTATGAGCTGTATGAGCTAGATGCGGAATTAG	2400
GTCACAAGGAGCTTGACTGGAAGATGACCATGAGTGGTGTGGGAAAATGC	2450
AGACAGGTAAATTAGTTGAAACAACCTGGCCTGCTTGAATTATTGTGTCTA	2500
TAAATTTTGACACCACCTTTTGTTCAGGTTGGTATCTCTGAAAGTGGA	2550
TAGATGAGGCAGTGCAAAAGCTATTAGCTCGTGGGTAAGGGAACCATCAT	2600
ACTTTATGGAATTCGTTTACTGCTACTTCGGCTAGGATTTAAGAAATGGA	2650
AATCACTTCAAGCATCATTAGTTAGGATCCTGAGAACTCAGGATGTTTTC	2700
TTATTCGTTATATAATAAGTCTTTTCATCAAGGAGTAACAAACAAAACCT	2750
GCACAATATTTGTGTGCTCACTGGCAAGGCATATATACCCAGCTAACCTT	2800
TGCTAGTTCACTGTAGTAACAGTTACGGATAATATATGTTTACTTGTATG	2850
TGGTACCCTCATTTTGTCTCTCATGGAGGCTTCAAGCCTTGTGTTGAAA	2900
CTGGATAGTTACATATGCTTCCAACAGAACTAGCATGCAGATTCATATG	2950
CTTTCCTATTCTACTAATTATGTATTGACACACTCGTTGTTTCTTTTGAA	3000
AGATATAAAGTTGGACGAATCGAGCAGCTAGAAACATCTGACCAAGCAAA	3050
AGCCAGAGGTGCTAATACTGTAAGTTTTCTTGGATAGGTCAAGGAGAGTG	3100
TTGCAGACTGTTTTTGATCATTTCTTTTTCTGTACATTACTTTCATGCTG	3150
TAATTAACCTCAATGGCTATTCTGGTCTGATTATCAGATAATTCCAAGGAA	3200
GCTAGTTCAGGTATTAACCTCCATCAACAGCAAGCGAGGGAAACATCGGGC	3250
CTGATGCCGTCCATCTTCTTGCTATAAAAGAGGTTTGTTATTTACTTATT	3300
TATCTTATCATGTTTCAGTTCATCCAAGTCCTGAAAAATTACACTCTTCTT	3350
TACCAATCTTCCATCAAGCTGTGTAAAGGATTTGGAATTAGAAAATCATT	3400
ATTTGATGCTTTGTTTTATATGCAAGAGGTTCCCTTGAAAAGATCTGTTT	3450
AAGATTCTTTGCACTTGAAAAATTCAATCTTTTTAAGTGAATCCCCTACT	3500
TTCTTACAATGATCATAGTCTGCAATTGCATGTCAAGTAATATCATTCCT	3550
TGTTACTGCATCCCCCTCTTTCTTAATGACCATTGTCTATGTTGTGTTTG	3600
TCTCGTGTGCTGGAGAAAATGATAGCTGATCCAAGCTGTACATTATCATG	3650
ATTAAGTAGCTGCTCAGGAATTGCCTTTGGTTACATTGCCTAATGGTTTG	3700
ATGTCAATTTTTCTTCTGAATCTTTATTTTAGATCAAAATGGAGCTACAA	3750
AAGTGTTCAACTGTGTATGGATTTGCTTTTGTTGACTGTGCTGCCTTGAG	3800
GTTTTGGGTTGGGTCCATCAGCGATGATGCATCATGTGCTGCTCTTGGAG	3850
CGTTATTGATGCAGGTAAGCAAGTGTATTCTGTATCTTATGTGTACCATG	3900
TGACTTCCTGTGCATATATTTGGGTTGCAGGAACTAATTCTGAATCACCA	3950
TTTGGTATGTTTTTTCCAGGTTTCTCAAAGGAAGTGTTATATGACAGTA	4000
AAGGTAACTGCTTGTATCGCCAGTTGTTTTGTTAAACAGAATTTAAGGT	4050
AAATGACACTGGTTAATTTAAAGTGCATACATGTTGAAATATTGCAGGGC	4100

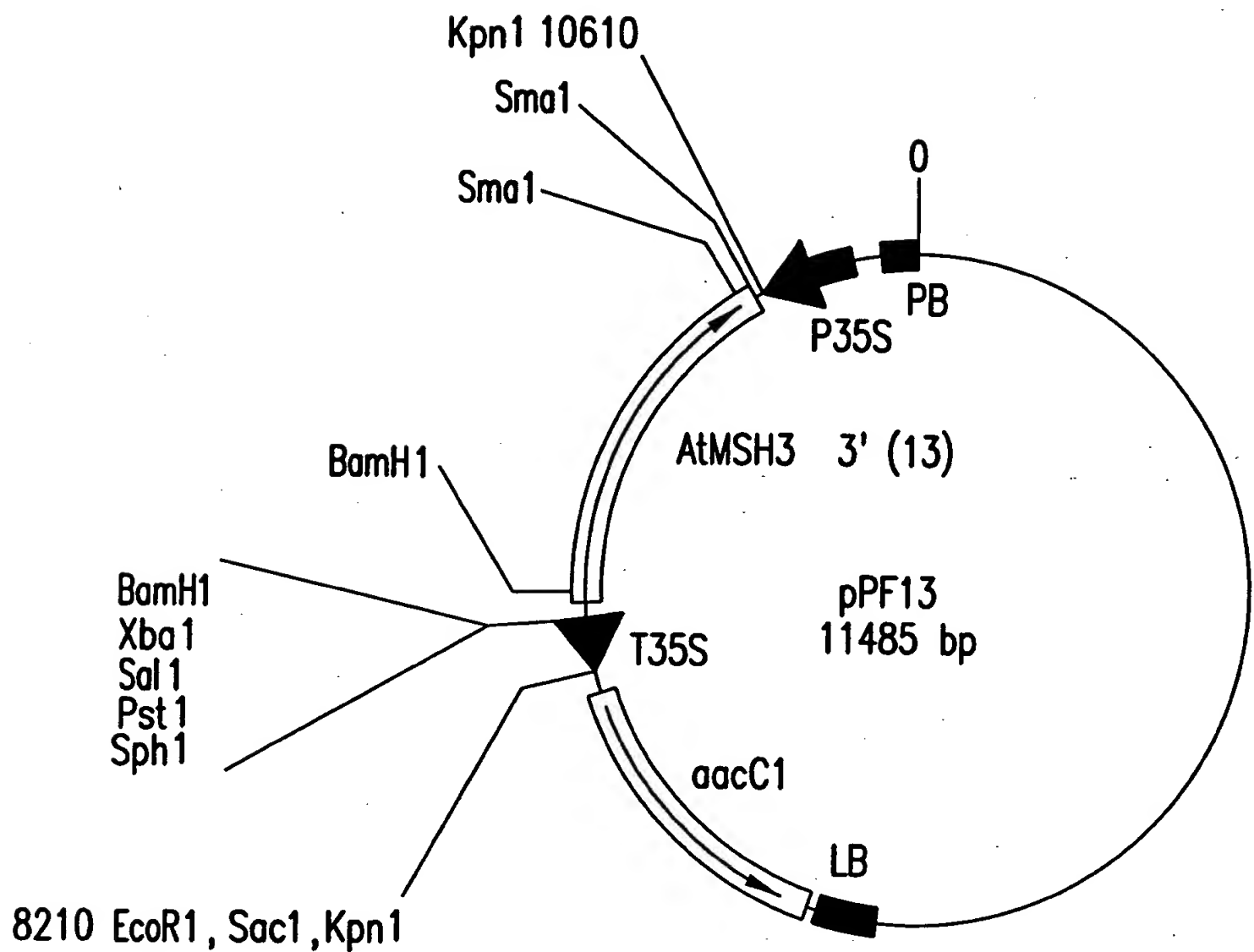
FIG. 11B

TATCAAGAGAAGCACAAAAGGCTCTAAGGAAATATACGTTGACAGGTACC	4150
ATTTTCAGTAGGCAAGCTAACTGACAATTTAACCGCTCACCGAATGATAGG	4200
TCTCTTAAACATTGCTAATGTAGATGATGTTTATGTTTCAATCTAATAGG	4250
GTCTACGGCGGTACAGTTGGCTCCAGTACCACAAGTAATGGGGGATACAG	4300
ATGCTGCTGGAGTTAGAAATATAATAGAATCTAACGGATACTTTAAAGGT	4350
TCTTCTGAATCATGGAAGTGTGCTGTTGATGGTCTAAATGAATGTGATGT	4400
TGCCCTTAGTGCTCTTGGAGAGCTAATTAATCATCTGTCTAGGCTAAAGG	4450
TGTGTTGGCTTGTTTAGTTTTGCTTTTCACAAATTAAGCAAAGGAACTT	4500
TTCATAACTTACAGTTTCTATCTACTTGCAGCTAGAAGATGTACTTAAGC	4550
ATGGGGATATTTTTCCATACCAAGTTTACAGGGGTTGTCTCAGAATTGAT	4600
GGCCAGACGATGGTAAATCTTGAGATATTTAACAATAGCTGTGATGGTGG	4650
TCCTTCAGGCAAGTGCATATTTCTTTTTTGATAACTTCAACTAGAGGGCA	4700
GACATAGAAGGAAAAATTCTAATACTTCGTACGGATCTCCAGTAAGTAAT	4750
AGCCGATTTTTGTTTACCTATGTAGGGACCTTGTAACAATATCTTGATAA	4800
CTGTGTTAGTCCAAGTGGTAAGCGACTCTTAAGGAATTGGATCTGCCATC	4850
CACTCAAAGATGTAGAAAGCATCAATAAACGGCTTGATGTAGTTGAAGAA	4900
TTACGGCAAACCTCAGAAAGTATGCAAATCACTGGCCAGTATCTCCACAA	4950
ACTTCCAGACTTAGAAAGACTGCTCGGACGCATCAAGTCTAGCGTTCGAT	5000
CATCAGCCTCTGTGTTGCCTGCTCTTCTGGGGAAAAAGTGCTGAAACAA	5050
CGAGTAAGTATCAATCACAAGTTTTCTGAGTAATGCCTTCCATGAGTAGT	5100
ATAGGACTAAACATTACGGGTCTAGCTAAAGACTGTTCTCCTTCTTTTG	5150
CAATGTCTGGTTATTCATTACATTTCTCTTAAGTATTGCATTGCAGGTT	5200
AAAGCATTTGGGCAAATTGTGAAAGGGTTCAGAAGTGGAATTGATCTGTT	5250
GTTGGCTCTACAGAAGGAATCAAATATGATGAGTTTGCTTTATAAACTCT	5300
GTAAACTTCCTATATTAGTAGGAAAAAGCGGGCTAGAGTTATTTCTTTCT	5350
CAATTCGAAGCAGCCATAGATAGCGACTTTCCAAATTATCAGGTGCCCAT	5400
CTATCTTTCATACTTTACAACAAAATGTCTGTCACTACTCAAAGCAATGC	5450
ATATGGCTTAGATCTCAACTCACACCCCGAGGATCCTAAAGGGATTTGCT	5500
TTTTATTCTAATGTTTTTGGATGGTTTGATTTATTTCTAACTTGAAGTT	5550
ATTAATCTTGTACCAGAACCAAGATGTGACAGATGAAAACGCTGAACTC	5600
TCACAATACTTATCGAACTTTTTATCGAAAGAGCAACTCAATGGTCTGAG	5650
GTCATTCACACCATAAGCTGCCTAGATGTCCTGAGATCTTTTGCAATCGC	5700
AGCAAGTCTCTGCTGGAAGCATGGCCAGGCCTGTTATTTTTCCCGAAT	5750
CAGAAGCTACAGATCAGAATCAGAAAACAAAAGGGCCAATACTTAAATC	5800
CAAGGACTATGGCATCCATTTGCAGTTGCAGCCGATGGTCAATTGCCTGT	5850
TCCGAATGATATACTCCTTGGCGAGGCTAGAAGAAGCAGTGGCAGCATT	5900
ATCCTCGGTCATTGTTACTGACGGGACCAACATGGGCGGAAAATCAACT	5950
CTTCTTCGTGCAACATGTCTGGCCGTTATCTTTGCCCAAGTTTGTATACT	6000
CGTTAGATAATTACTCTATTCTTTGCAATCAGTTCTTCAACATGAATAAT	6050
AAATTCTGTTTTCTGTCTGCAGCTTGGCTGCTACGTGCCGTGTGAGTCTT	6100
GCGAAATCTCCCTCGTGGATACTATCTTCACAAGGCTTGGCGCATCTGAT	6150

FIG. 11C

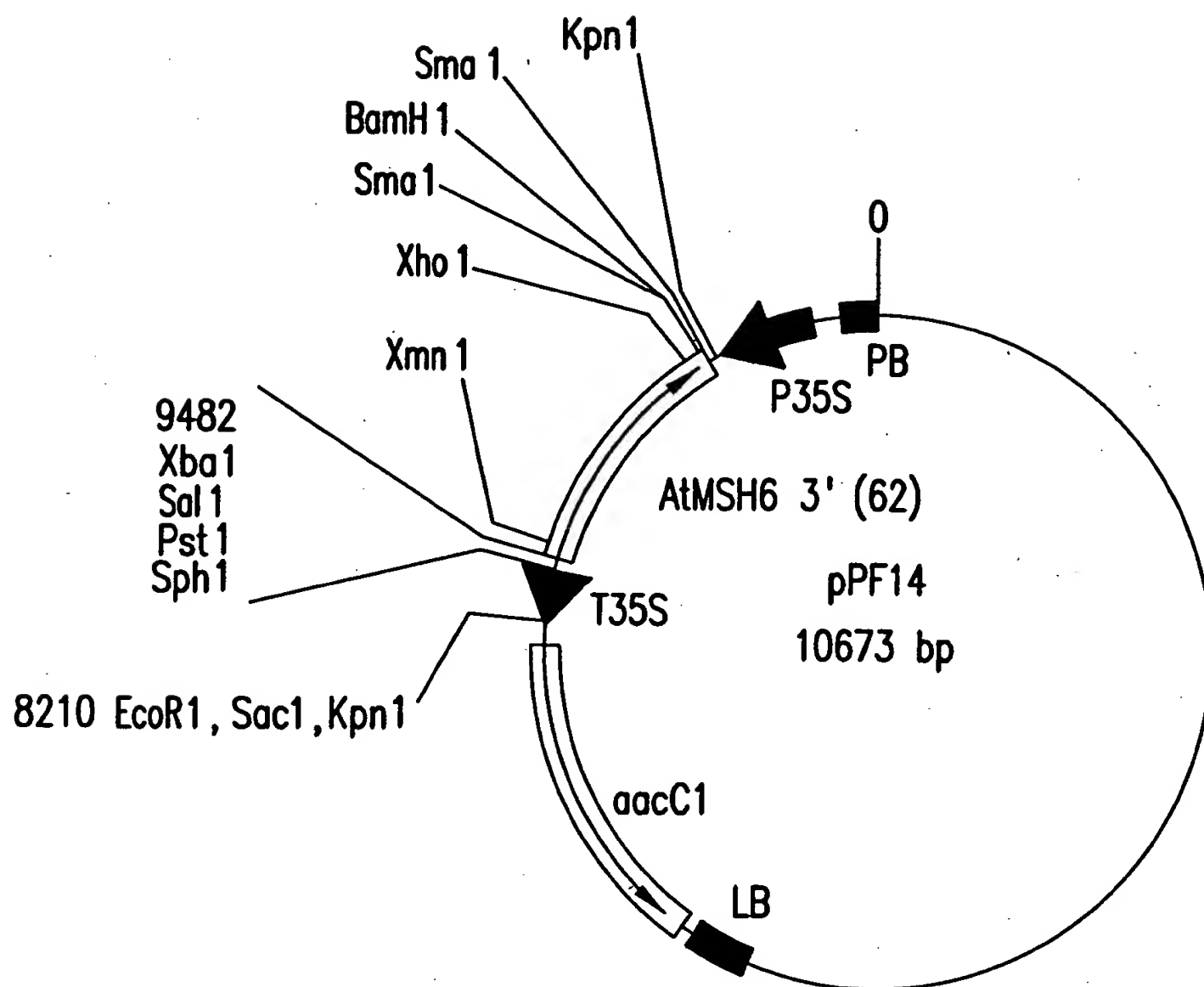
AGAATCATGACAGGAGAGAGTAAGTTTTGTTCTCAAATACCAATTCCTC	6200
GAACTATTTACTCAGATTTTGTCTGATTGGACAAGGTGGTTTTGCTTTTT	6250
TTTAGGTACCTTTTTGGTAGAATGCACTGAGACAGCGTCAGTTCTTCAGA	6300
ATGCAACTCAGGATTCCTAGTAATCCTTGACGAACTGGGCAGAGGAACT	6350
AGTACTTTCGATGGATACGCCATTGCATACTCGGTAACCTGCTCTTCTCC	6400
TTCAACTTATACTTGTGATCAACAAAAACATGCAATTCATTTTGCTGAA	6450
ACTTATTGATTTATATCAGGTTTTTCGTACCTGGTAGAGAAAGTTCAAT	6500
GTCGGATGCTCTTTGCAACACATTACCACCCTCTCACCAAGGAATTCGCG	6550
TCTCACCCACGTGTCACCTCGAAACACATGGCTTGCGCATTCAAATCAAG	6600
ATCTGATTATCAACCACGTGGTTGTGATCAAGACCTAGTGTTCTTGTACC	6650
GTTTAACCGAGGGAGCTTGTCTGAGAGCTACGGACTTCAAGTGGCACTC	6700
ATGGCTGGAATACCAAACCAAGTGGTTGAAACAGCATCAGGTGCTGCTCA	6750
AGCCATGAAGAGATCAATTGGGGAAAACCTTCAAGTCAAGTGAGCTAAGAT	6800
CTGAGTTCTCAAGTCTGCATGAAGACTGGCTCAAGTCATTGGTGGGTATT	6850
TCTCGAGTCGCCCACAACAATGCCCCATTGGCGAAGATGACTACGACAC	6900
TTTGTTTTGCTTATGGCATGAGATCAAATCCTCTTACTGTGTTCCCAAAT	6950
AAATGGCTATGACATAACACTATCTGAAGCTCGTTAAGTCTTTTGCTTCT	7000
CTGATGTTTATTCCTCTTAAAAAATGCTTATATATCAAAAAATTGTTTCC	7050
TCGATTATAACAAGATTATATATGTATCTGTGCGTTTAGCTATGGTATAT	7100
AATATATGTATGTTTCATGAGATTGGTCAAGAGAAATACTCACAAACAGTA	7150
TATTAAGAAGGAAATATGTTTATGCATTAATTTAAGTTTCAAGATAAACT	7200
GCAAATAACCTCGACTAAAGTTGCAAAGACCAAACACAAATTACAAAACCT	7250
TATAAGACTTAAGTTCTGAATTCCTAAAACCAAAAAAAAAAACAGAACA	7300
TATTTTGTTGCATCTACAAACAACACAAACCTACATAGTTTATAACTTAC	7350
TCATCACTGAGATTAACATCAGAATCATTCTCCATTTCTTCATCTTCACT	7400
CTCATCATCATCACCACCACCATGATGATTCTCCTCCTCTTCACGTAACC	7450
TAGCAATCTCACTCTGAGCTCTATCAACAATCTGCTTCTTCTGCAACTCC	7500
AAATCTCTCTGAAAATCAGCTCTCATCTTCTCCAACCTCCTTCATTTGCTC	7550
TTTCTTACTCTTCTCCATCTTCTCATAAACCTTCCCAAACCTCTCAACAG	7600
AATCCGCCAACATCTTATACGAAGCAGCGTCATTAACCTTCTTCTCTCG	7650
TACTCAACCTCATCATCCTCATCCTCCTCCTCTTCAGAATCACCAGGACT	7700
ATCCATCATCTCATCAAACCCATTAGACTTATCTAAATAAACCTTAGTGT	7750
TCATAAACACAAACTCACCTGAATCAACACCACAAGCTAAACCTAAATCC	7800
GACTTGGGCGAAACACAAAGCAACATATCCAACCTTATTGAAAAACGACCA	7850
TTTACTTGAACCTAAACCTGATTTCTCAACCTTAATCTTCTCTTTTCTAT	7900
ACTTCCTCTTCAAGTCATCAATCATTCTCCTACATTGCGTCTCAGATTTT	7950
TCCATCCTTAGCTCCTCACTCACTTTCTCAGCTACTTCATTCCAATCCTC	8000
GTTCTCAAACTCCTTCTACCCAATTGCAAAAACCTATCTCCCCAAACTT	8050
CAAGCAACACAA	8062

FIG. 11D



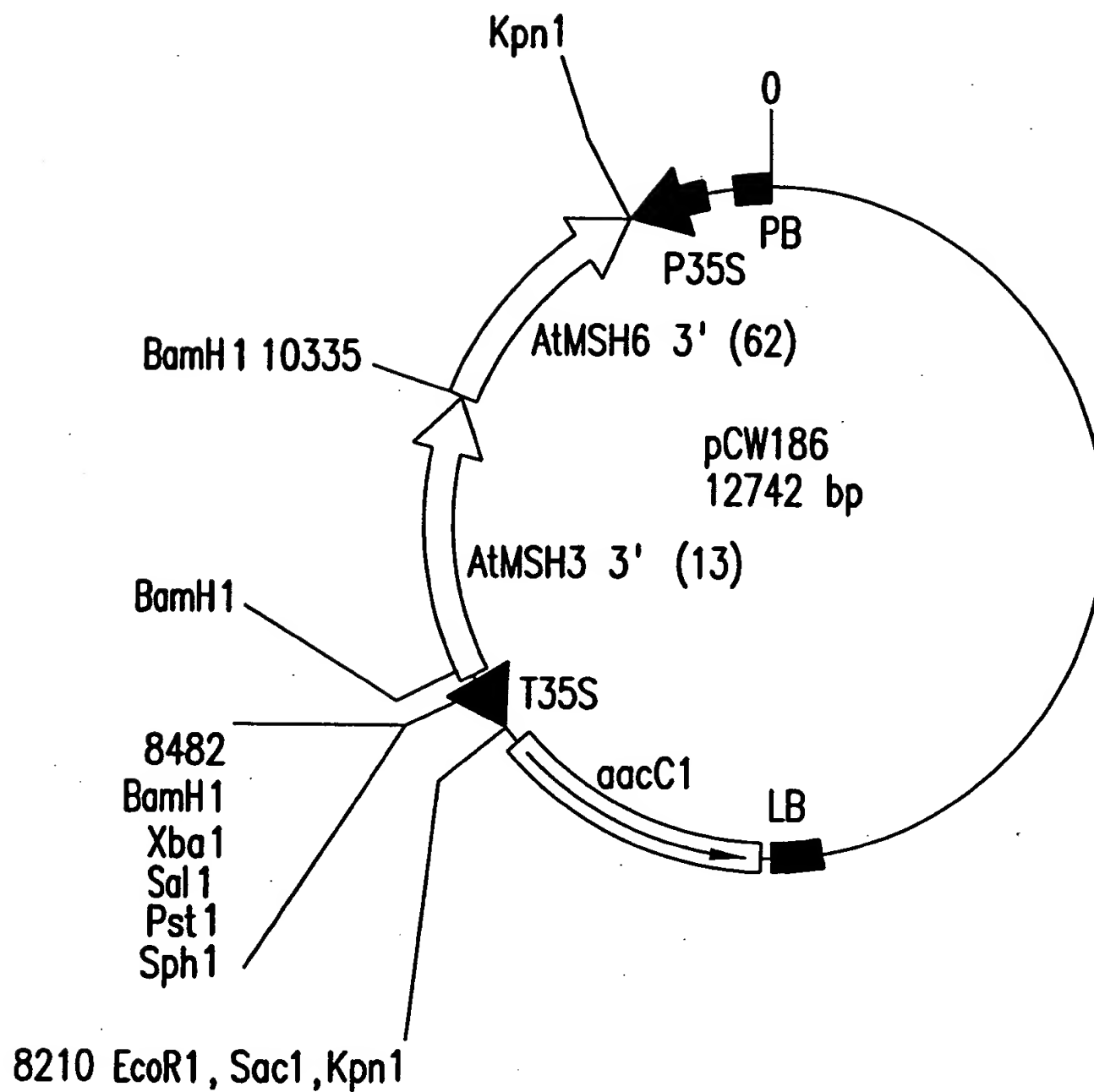
COMMENTS/REFERENCES: AtMSH3 3' SIDE ANTISENSE: AtMSH3 3' (13=2104bp) FROM pUC18/13 Sal1/Sst1/T4 INTO pCW164 BamH1/T4 IN AGROBACTERIUM LBA4404

FIG.12



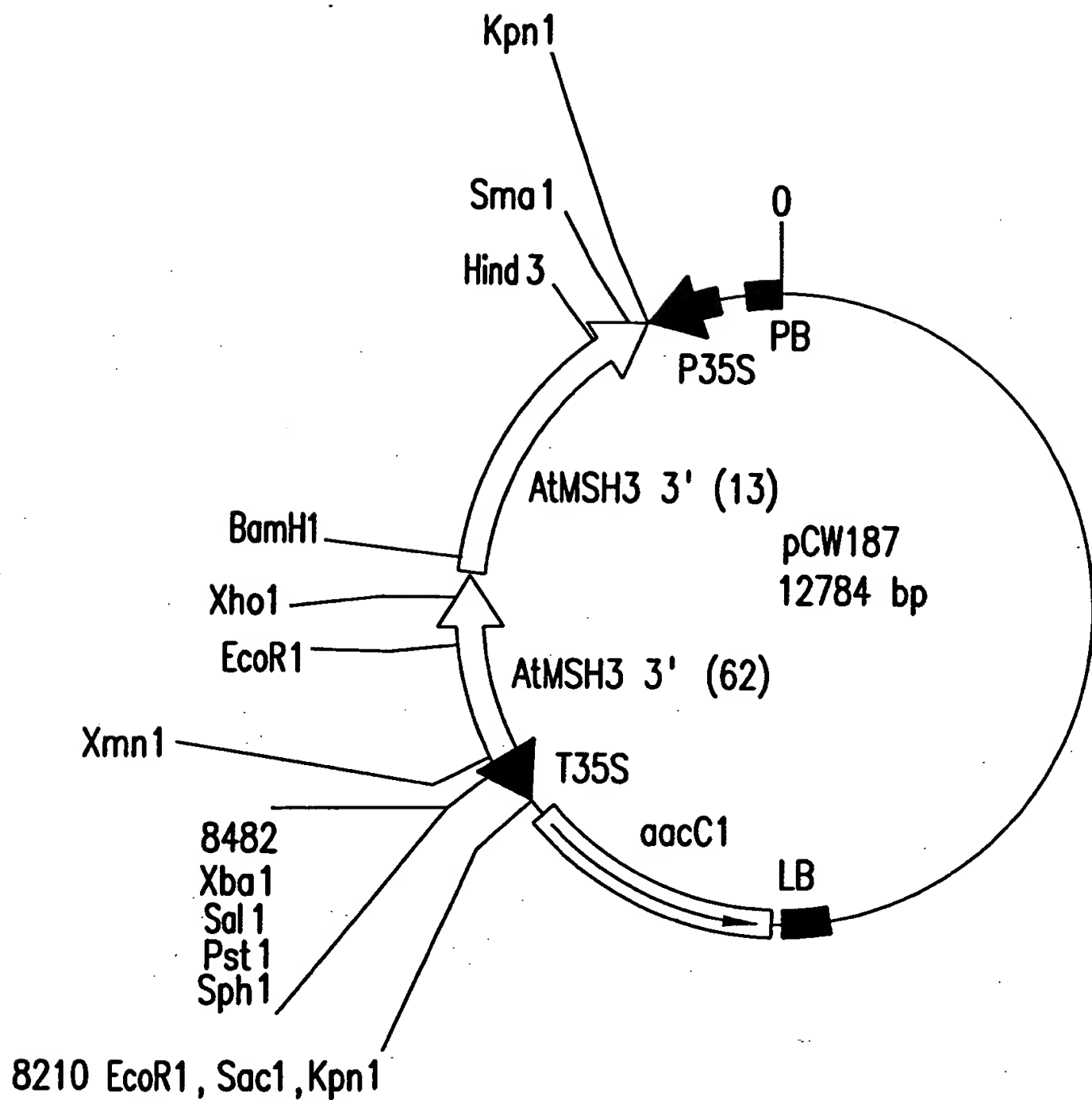
COMMENTS/REFERENCES: AtMSH6 (S8) 3' SIDE ANTISENS: 62 Sal1/Sst1/T4 (1379bp)
 INTO pCW164 BamH1/T4

FIG.13



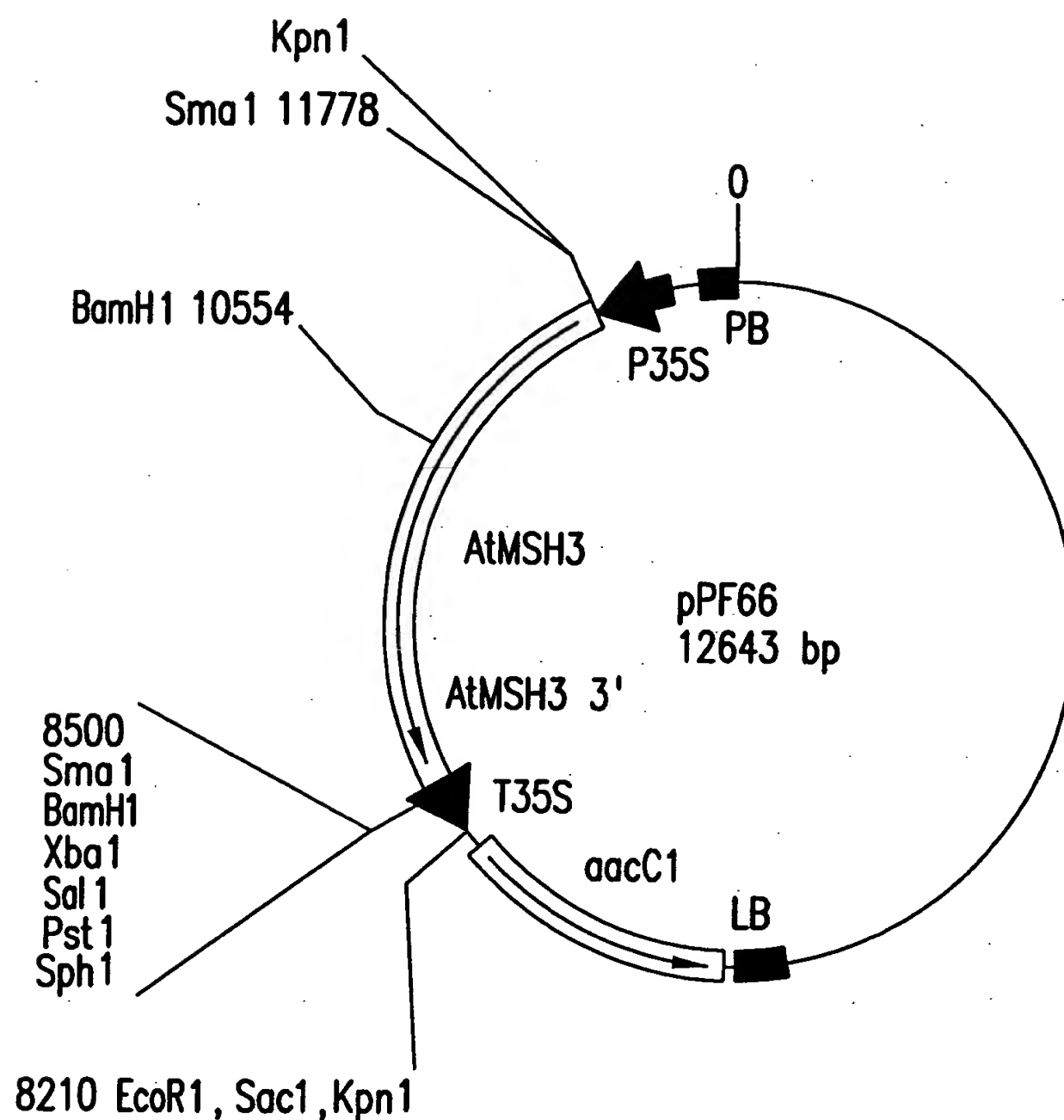
COMMENTS/REFERENCES: AtMSH6 3' /AtMSH3 3' ANTISENSE: AtMSH6 (S8) 3' SIDE (62=1379bp)
Sal1/Sst1/T4 INTO pPF13 (pCW164 AtMSH3 (S5) 3' SIDE (13=2104) ANTISENS)/Sma1.
IN LB4404

FIG.14



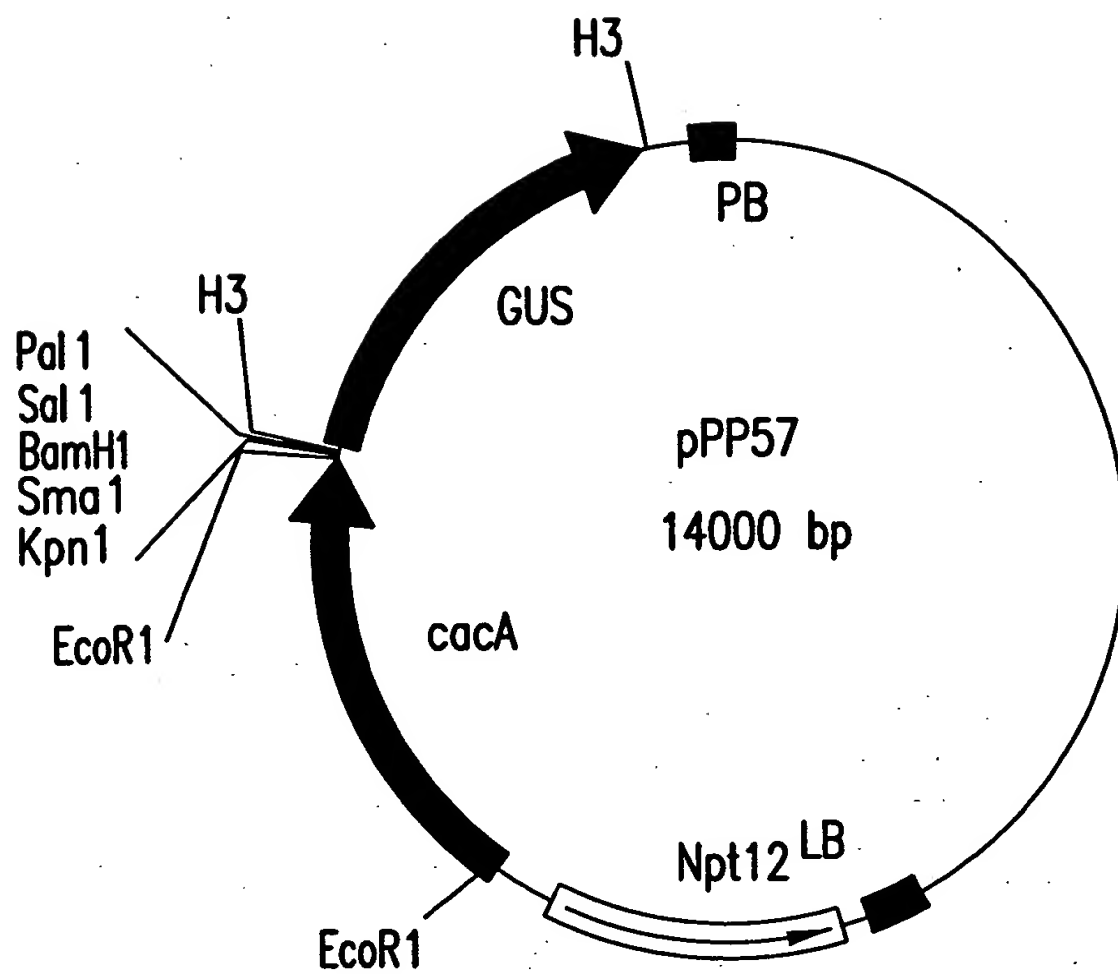
COMMENTS/REFERENCES: AtMSH3 3' /AtMSH6 3' ANTISENS (D): AtMSH3 (S5) 3' SIDE (13=2104bp) Sal1/Sst1/T4 INTO pPF14 (AtMSH6 (S8) 3' SIDE (62=1379bp) ANTISENSE INTO pCW164)/Sma1. IN LBA4404

FIG.15



COMMENTS/REFERENCES: AtMSH3 (S8) COMPLETE, SENSE ORIENTATION: pPF26 (3342bp)
Sma1 INTO pCW164 Sma1

FIG.16



COMMENTS/REFERENCES: pP2P111 WITH *codA* EcoR1 CASSETTE IN EcoR1 SITE AND Hind3 GUS CASSETTE IN Hind3 SITE KanR. ALL GENES UNDER PROMOTER/TERMINATOR 35S

FIG.17

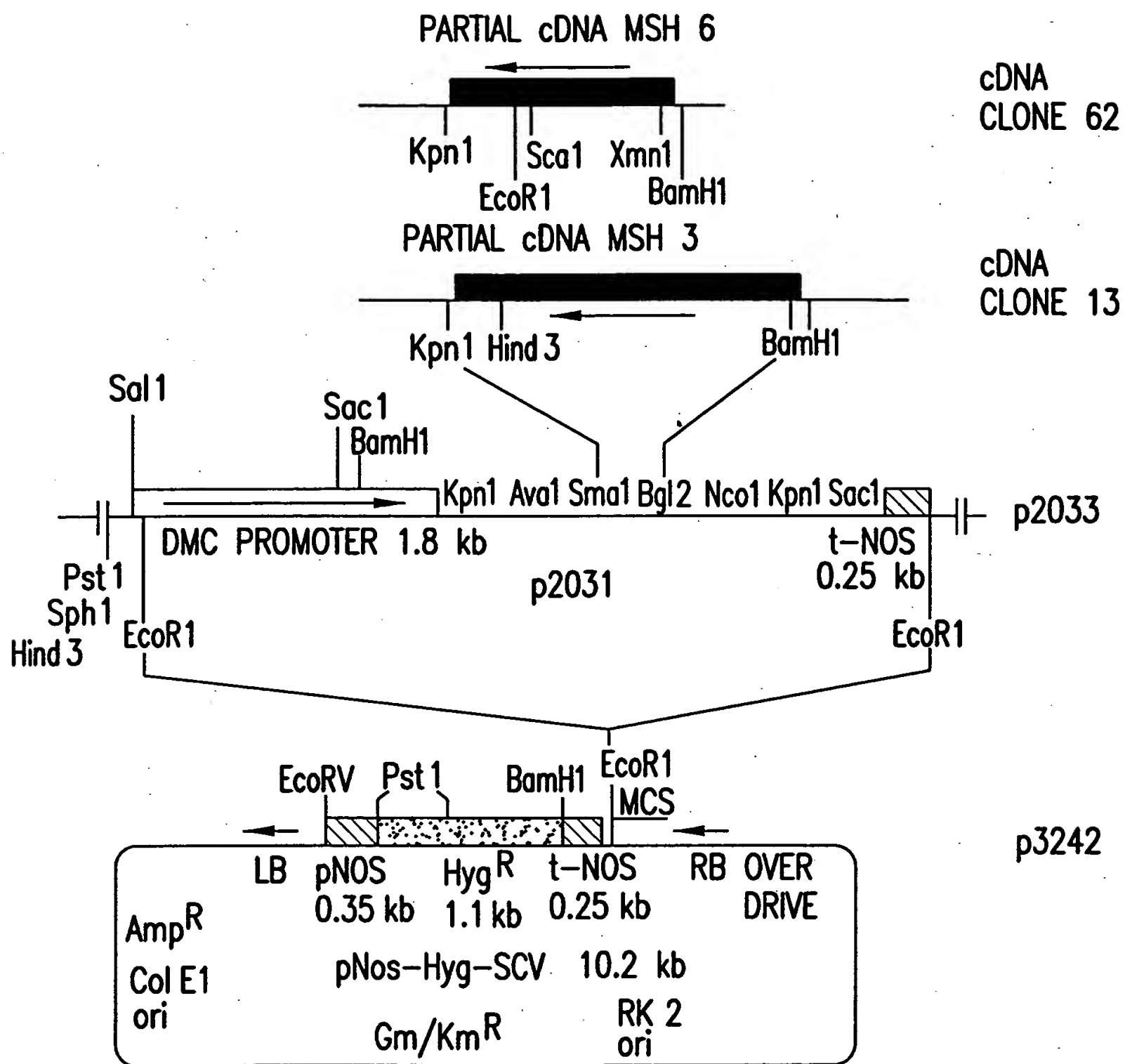


FIG.18

p3243

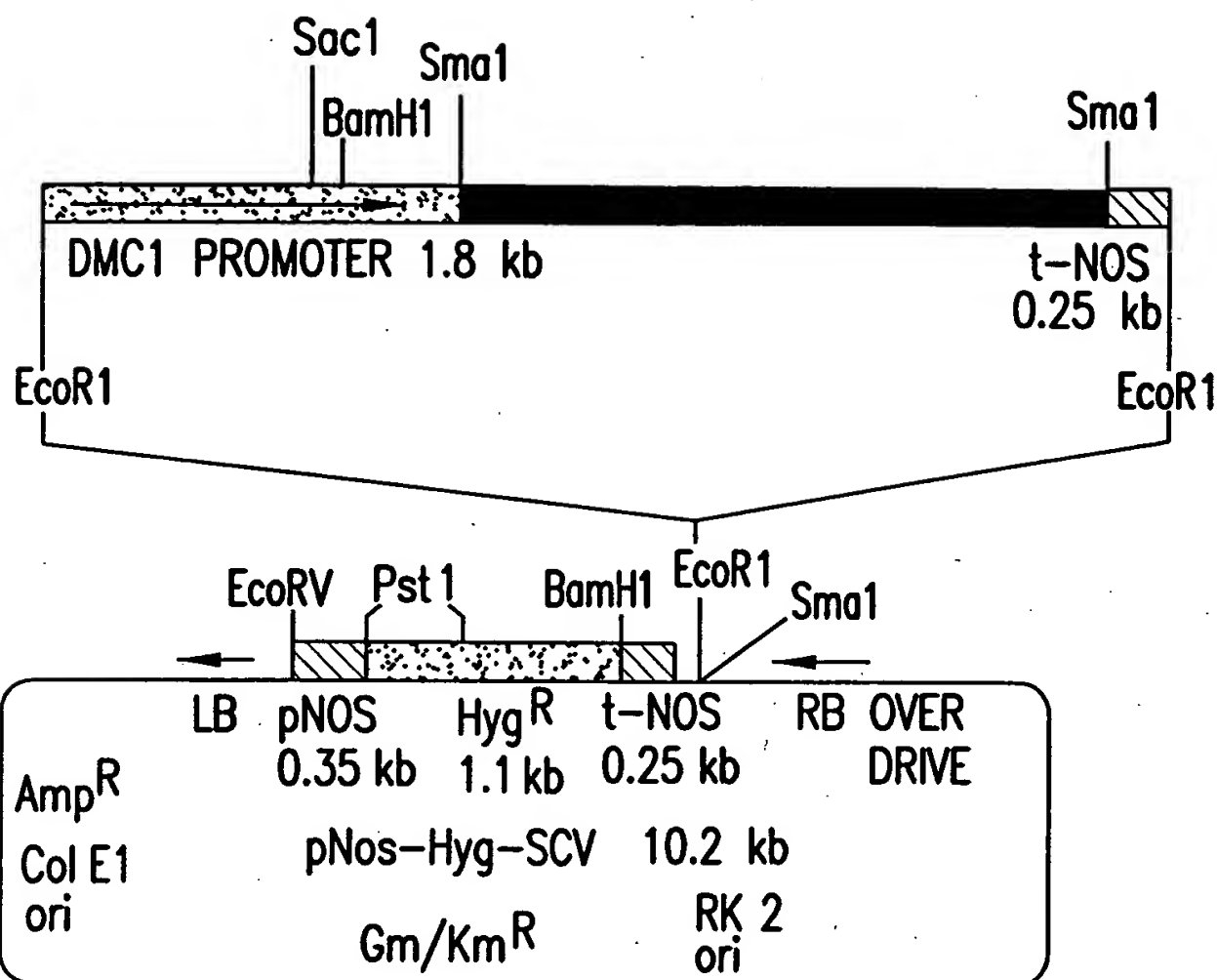


FIG.19